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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

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ANTI-BACTERIAL VACCINE COMPOSITIONS

This application is a continuation-in-part of U.S. Patent Application Serial No: 09/545,199, filed April 6, 2000, which claims benefit of U.S. Provisional Patent Application Serial Nos. 60/153,453, filed September 10, 1999 and 60/128,689, filed April 9, 1999.

FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurellaceae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe

climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

P. multocida strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgaris*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

At least eleven serotypes (1, 2, 5-9, 12-14 and 16) have been demonstrated within *Mannheimia* [*Pasteurella*] *haemolytica* [Angen, *et al.*, *Vet Microbiol* 65(4):283-90 (1999)], a *Pasteurellaceae* species which is responsible for serious outbreaks of acute pneumonia in neonatal, weaned, growing and adult lambs, calves, and goats [Ackermann, *et al.*, *Microbes Infect* 2(9):1079-88 (2000)]. Transportation, viral infections, overcrowding, and other stressful conditions predispose animals to *M. haemolytica* infection [Ackermann, *et al.*, *supra.*] The leukotoxin (Lkt) of *M. haemolytica* is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever [Highlander, *et al.*, *Infect Immun* 68(7):3916-22 (2000)] as well as lung injury in bovine pneumonic pasteurellosis [Jeyaseelan, *et al.*, *Microb Pathog* 30(2):59-69 (2001)]. Lkt is a pore-forming exotoxin that has the unique property of inducing cytolysis only in ruminant leukocytes and platelets [Jeyaseelan, *et al.*, (2001), *supra.*]. Cytolysis of many cell types is mediated by arachidonic acid (AA) and its generation by phospholipases is regulated by G-protein-coupled receptors [Jeyaseelan, *et al.*, (2001) *supra.*] Recent studies indicate that *M. haemolytica* Lkt binds to bovine CD18, the common subunit of all beta2 integrins [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)]. It has also been shown that LFA-1 is a Lkt receptor, Lkt binding to LFA-1 is not target cell specific, Lkt binding to bovine LFA-1 correlates with calcium elevation and cytolysis, and bovine LFA-1 expression correlates with the magnitude of Lkt-induced target cell cytolysis [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent

serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet Res.* 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the
5 ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

10 Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *Pasteurellaceae* serotypes. There further exists a need to identify
15 attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for
20 production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are
25 not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H.*
30 *parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H.*

paraphrohaemolyticus, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*,
H. somnus, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*,
P. avium (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. (Mannheimia)*
haemolytica, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P.*
5 *pneumotropica*, *P. stomatis*, *P. volantium* (*H. parainfluenzae*), *P. volantium*,
Pasteurella species A, *Pasteurella* species B, and *Haemophilus*
paraphrohaemolyticus. Preferably, vaccine compositions comprise attenuated
Pasteurella (Mannheimia) haemolytica, *Actinobacillus pleuropneumoniae*,
Haemophilus somnus, or *Pasteurella multocida* bacteria. In a most preferred
10 embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella*
multocida and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial
 organisms containing a functional mutation in a gene sequence represented by any one
 of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51,
 15 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110,
 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142,
 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and
 174, or species homologs thereof, wherein the mutation inhibits or abolishes
 expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide
 20 encoded by a gene); said functional mutation resulting in attenuated virulence of the
 bacterial strain. Functional mutations that modulate (*i.e.*, increase or decrease)
 expression and/or biological activity of a gene product include insertions or deletions
 in the protein coding region of the gene itself or in sequences responsible for, or
 involved in, control of gene expression. Deletion mutants include those wherein all or
 25 part of a specific gene sequence is deleted. Also contemplated are compositions, and
 preferably vaccine compositions, comprising mutated and attenuated gram negative
 bacterial organisms, optionally comprising a suitable adjuvant and/or a
 pharmaceutically acceptable diluent or carrier. In order for a modified strain to be
 effective in a vaccine formulation, the attenuation must be significant enough to

prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, as well as related gene sequences from other

gram negative bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit, and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs, including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that include CDR sequences which specifically recognize a polypeptide of the invention. The invention also provides anti-idiotypic antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

5

DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in virulence by subsequent determination of an approximate LD₅₀ for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences. Knowledge of the virulence genes in these species permitted identification of species homologs in *P. (Mannheimia) haemolytica*.

The identification of bacterial, and more particularly *P. multocida* *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes provides for microorganisms exhibiting reduced virulence (i.e., attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple

mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* can provide information regarding similar genes in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallinarum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica*, and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. (Mannheimia) haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exxB*, *atpG*, *pnp*, *guaB* and *yjgF*.

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is removed, thereby precluding the possibility that the bacteria will revert to a virulent state.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reyrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome with a marker gene, such as green fluorescent protein (GFP), β -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*. An expression cassette, containing a promoter active in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of

such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica* or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida* virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *P. (Mannheimia) haemolytica* virulence gene products are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,

55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, according to Watson-Crick base pairing rules for DNA. Also preferred are

5 polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof. The invention further embraces
10 species, preferably bacterial, homologs of the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related
15 bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57,
20 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, and species homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

25 The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116,
30 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146,

148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer
5 comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley &
10 Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New
15 York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression
20 control DNA sequence and a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after
25 the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in
30 *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of

E. coli or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention. Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-

1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *BioTechnology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172 and 174, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of: a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174 and species homologs thereof; b) DNA molecules encoding *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof; and c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least

about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

Table A
Conservative Substitutions I

<u>SIDE CHAIN CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	Non-polar
	G A P I L V
	Polar - uncharged
	C S T M N Q
	Polar - charged
	D E K R
Aromatic	H F W Y
Other	N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more

of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

Table B
Conservative Substitutions II

<u>SIDE CHAIN</u>	
<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Non-polar (hydrophobic)	
A. Aliphatic:	A L I V P
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	S T Y
B. Amides:	N Q
C. Sulfhydryl:	C
D. Borderline:	G
Positively Charged (Basic):	K R H
Negatively Charged (Acidic):	D E

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see

Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as
5 defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a
10 polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which
15 specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence
20 family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillito, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation
25 of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either
30

exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

5 Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of
10 proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

 The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997).
15 Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization
20 include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

25 The identification of *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1,
30 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68,

70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof (i.e., the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based

on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

5 The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When
10 the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction
15 with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding
20 partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

25 Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical
30 libraries consist of structural analogs of known compounds or compounds that are

identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246 (1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of

which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety

of proteins, and it is not even necessary to know the identity or function of the second binding protein. The system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

5 Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two
10 states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined
15 by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

20 Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The
25 specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention. For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.*, trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.*, mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.*, extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.*, OK432), Biostim™ (*e.g.*, 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Ammycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the

recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, *e.g.*, in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to screening for *P. multocida* mutants. Example 3 addresses methods to determine

virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge. Example 12 describes identification of species homolog virulence genes in *P. (Mannheimia) haemolytica*.

Example 1

Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al.*, *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al.*, *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]₃₅ sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *Kpn*I restriction site in the multiple cloning region and then to introduce a new *Kpn*I site in the mini-Tn10 region. The plasmid was digested with *Kpn*I and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to

produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E. coli* DH5 α : λ pir for amplification. *E. coli* DH5 α : (λ pir ϕ 80dlacZ Δ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r_k⁻, m_k⁻, supE44, relA1, deoR, Δ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using

5 QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *SfiI* which cuts at a unique site within the mini-Tn10 transposable element. A *SfiI-KpnI-SfiI* adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all

10 other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCTT SEQ ID NO: 86

15 TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *KpnI* site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under

20 conditions including 250 μ M each dNTP, 1.5 mM Mg(OAc)₂, 100 pmol each primer TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

25 TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

30 5'-CTAGGTACCTACAACCTCAAGCTT-[NK]₃₅-
AAGCTTGGTTAGAAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *KpnI* and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *KpnI* and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 α : λ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100 μ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems), 200 μ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl₂, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN).

Approximately 15 ng of the primary product was labeled in a 50 μ l PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

5 TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

 TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

10 PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *Hind*III in a total reaction volume of 90 μ l and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved

15 and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

 Dot blots were prepared using a Hybond[®]-N⁺ membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal

20 vacuum using a Minifold I[™] Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 μ l of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 μ l of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and

25 hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate [NK]₃₃ sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into *E.coli* S17-1:λpir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96 *E.coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO₂ when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir/pTEF1:[NK]₃₃ clone and the TF5 strain to late log phase. Fifty μl of culture for each tagged-pTEF-1 clone was mixed with 200 μl of the TF5 culture and 50 μl of each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates

containing 100 mM IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN⁵⁰K¹⁰⁰ plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 µl BHIN⁵⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

Example 2

Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN⁵⁰K⁵⁰). Plates were incubated without shaking overnight at 37°C in 5% CO₂. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar) containing 100 µl of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD₅₄₀ was monitored using a micro-titer plate reader. At an OD₅₄₀ of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10⁴, 10⁵, 10⁶ CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized

in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from 10^{-2} to 10^{-5} were prepared and plated onto BHI⁵⁰K⁵⁰ plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to
5 prepare genomic DNA according to a previously described protocol [Wilson, *In F. M. Ausubel, et al.* (ed.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual
10 inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 µg of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the
15 host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were
20 selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

Example 3

Determination of Virulence for *P. multocida* Candidate Mutants

Each potential mutant which exhibited reduced recovery from splenic
25 tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO₂ at 37°C. Approximately six colonies of each
30 mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with 10^2 , 10^3 , 10^4

and 10^3 CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the LD_{50} for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate LD_{50} of at least 10 fold higher than the wild type strain. The clones and their approximate LD_{50} values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to LD_{50} values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice ($n = 5$ to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the LD_{50} of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

Table 1
***P. multocida* Virulence Genes**

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD_{50}
-	wild type	-	0/0	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3×10^6
11	PM1D1	dstB	10/10, 5/10	10/10, 5/5	8.4×10^4
3	PM1BD7	atpG	5/5, 10/10	10/10	$>3 \times 10^5$
74	PM1BE11	yhjJ (HI0145)	10/10	5/10	$>2 \times 10^5$
70	PM1BF6	yabK (HI1020)	3/5, 8/10	9/9	$>2 \times 10^5$
19	PM2G8	flaC	4/5, 9/10	9/9	$>4 \times 10^5$
76	PM3C9	yiaO (HI0146)	3/5		$>6 \times 10^5$
118	PM3G11	UnkO	4/5, 10/10	10/10	$>3 \times 10^5$
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	flaB (flaB2)	2/5, 10/10, 9/10	10/10, 9/9	$>3 \times 10^6$
9	PM4G10-T9	dnaA	4/5		$>5 \times 10^5$
1	PM4D5-T5	atpB	5/5		$>4 \times 10^5$
53	PM4D5-T1	UnkC2	5/5		$>4 \times 10^5$
15	PM4F2	flaB (flaB1)	3/5, 6/10, 10/10	6/6, 10/10	$>3 \times 10^5$
41	PM5F7	rneB	4/5		1×10^3
7	PM5E2	devB	0/5, 3/10	2/3	ND
68	PM6H5-T1	xyzA	5/5		$>3 \times 10^5$
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	$>3 \times 10^5$
108	PM7D12	pmp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		$>6 \times 10^5$

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	LD ₅₀
37	PM8C1-T3	mgIB	5/5		~6 x 10 ⁵
58	PM8C1R1-T6	UnkD1	5/5		~6 x 10 ⁵
43	PM10H7	purF (H11707)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 10 ⁵
23	PM10H10-T2	H11501	5/5		>1 x 10 ⁴
72	PM11G8-T2	ygiK	5/5		>2.4 x 10 ³
21	PM11G8-T4	greA	5/5		>2.4 x 10 ³
84	PM12H6	yyam (H10687)	3/5, 0/10		~2.2 x 10 ³
33	PM15G8-T2	kdtB	5/5		>1.2 x 10 ⁵
116	PM15G8-T1	UnkK	5/5		>1.2 x 10 ⁵
104	PM16G11-T1	hmbR	3/5		>1.9 x 10 ⁵
29	PM16G11-T2	hxaC	3/5		>1.9 x 10 ⁵
35	PM16H8	lglC	5/5, 10/10	10/10	>2.4 x 10 ⁵
80	PM16H3	yleA (H10019)	5/5, 10/10		>2.0 x 10 ⁵
49	PM17H6-T1	sopE	4/5		~6 x 10 ⁵
120	PM17H6	UnkP	4/5		~6 x 10 ⁵
5	PM18F5-T8	cap5E	5/5		>2.4 x 10 ⁵
82	PM18F5-T10	yoyB (H10345)	5/5		>2.4 x 10 ⁵
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 10 ⁵
112	PM19D4	rci	5/5, 8/10	8/8	~1.6 x 10 ⁵
39	PM20A12	mioC (H10669)	3/5, 8/10	8/8	~2 x 10 ⁴
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 10 ⁶

Example 4

Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32 GGCAGAGCATTACGCTGAC SEQ ID NO: 95
TEF-40 GTACCGGCCAGGCGGCCACGCGTATTC SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for putative interrupted open reading frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison] were used to search for homologous sequences in currently available databases.

In 37% of the clones that were identified as being attenuated, there were multiple insertions of the mini-Tn10 transposable element. Each insertion including its flanking sequence was cloned individually into pGP704 and mated into the wild-type strain to produce new mutants of *P. multocida*, each carrying only one of the multiple original insertions. Individual mutants were retested individually to determine the insertion responsible for the attenuated phenotype. The nucleotide sequence of the disrupted, predicted open reading frame was determined by sequencing both strands, and the predicted amino acid sequence was used to search currently available databases for similar sequences. Sequences either matched known genes, unknown genes, and hypothetical open reading frames previously sequenced or did not match any previously identified sequence. For those genes having homology to previously identified sequences, potential functions were assigned as set out in Table 1.

25

Example 5 Identification of Related Genes in Other Species

In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P. multocida* *atpG* gene. This result suggested the presence in other bacterial species of

30

homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae atpG* gene as a probe.

Actinobacillus pleuropneumoniae, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *EcoRI* and *HindIII* for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N⁺) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atgG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X

SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

- 5 Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *EcoRI* digested DNA. Two bands were detected using *EcoRI* digested DNA from *Pasteurella multocida*.

Example 6

10 Construction of a Library of Tagged-Transposon *P. multocida* Mutants

- Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1: λ pir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]₃₅) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10 μ g/ml B-nicotinamide adenine dinucleotide (V¹⁰), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO₂ when grown on plates. *E. coli* S17-1: λ pir (λ pir, *recA*, *thi*, *pro*, *hsdR*(r₋m₊), RP4-2, (Tc^R::Mu), (Km^R::Tn7), [Tm^R], [Sm^R]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100 μ g/ml ampicillin (Sigma), 50 μ g/ml nalidixic acid (N⁵⁰)(Sigma), and 50 (K⁵⁰) or 100 (K¹⁰⁰) μ g/ml of kanamycin (Sigma).

- 25 Matings were set up by growing each *E. coli* S17-1: λ pir/pTEF1:[NK]₃₅ clone and the AP225 strain to late log phase. A 50 μ l aliquot of culture for each tagged-pTEF-1 clone was mixed with 150 μ l of the APP225 culture, and then 50 μ l of each mating mixture was spotted onto 0.22 μ M filters previously placed onto BHIV¹⁰ plates containing 100 μ M IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 2 ml of PBS and 200 μ l of each was plated onto BHIV¹⁰N⁵⁰K¹⁰⁰ plates. After selective

overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 μ l BHIV¹⁰N³⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 μ l of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

Example 7 **Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants**

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20 μ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180 μ l of BHIV¹⁰N³⁰K⁵⁰. Plates were incubated without shaking overnight at 37°C in

5% CO₂. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of BHIV¹⁰ per well and incubating at 37°C with shaking at 150 rpm. The OD₅₆₂ was monitored using a microtiter plate reader. At an OD₅₆₂ of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter plate. The culture was diluted appropriately in BHI to approximately 2 X 10⁶ CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in dilutions ranging from 10⁻² to 10⁻⁵ onto BHIV¹⁰N¹⁵⁰K⁵⁰ plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In Ausubel, et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the 10⁸ CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also used for inverse PCR reactions and sequencing.

TEF69	GACGTTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTTAAC	SEQ ID NO: 168

5

The labeled PCR product was then digested with *HindIII* to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The $LCPS_{input} / LCPS_{recovered}$ ratio for each mutant was used to determine mutants likely to be attenuated.

Clones selected as being present in the input pool but highly reduced in
15 the recovered pool were selected for further study. Additional clones with
questionable input/recovered ratios were also selected after visually evaluating films
made from the dot blots. A total of 110 clones were selected.

20 **Example 8**
Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Sequencer 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haebertli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

Table 2
***A. pleuropneumoniae* Open Reading Frames**

	<u>Complete Open Reading Frame</u>	<u>NO Start Codon - Stop Codon</u>		
10	atpH	SEQ ID NO: 134	dksA	SEQ ID NO: 136
	aptG	SEQ ID NO: 132	dnaK	SEQ ID NO: 138
	exbB	SEQ ID NO: 140	HI0379	SEQ ID NO: 144
	OmpP5	SEQ ID NO: 152		
	OmpP5-2	SEQ ID NO: 150		
15	tig	SEQ ID NO: 160	<u>NO Start Codon - NO Stop Codon</u>	
	fkpA	SEQ ID NO: 142	pnp	SEQ ID NO: 154
	hupA	SEQ ID NO: 146	apvA-or 1	SEQ ID NO: 122
	rpmF	SEQ ID NO: 158	apvA-or 2	SEQ ID NO: 124
			apvB	SEQ ID NO: 126
			apvD	SEQ ID NO: 130
	<u>Start Codon - NO Stop Codon</u>			
20	lpdA	SEQ ID NO: 148	<u>RNA or Noncoding Sequences</u>	
	potD	SEQ ID NO: 156	tRNA-leu	SEQ ID NO: 162
	yaeE	SEQ ID NO: 164	tRNA-glu	SEQ ID NO: 163
	apvC	SEQ ID NO: 128		

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

Example 9
Competition Challenge of *A. pleuropneumoniae*
Mutants with Wild Type APP225

A representative clone from each of the unique attenuated mutant groups identified above that was absent or highly reduced in the recovered population was isolated from the original pool plate and used in a competition challenge experiment with the wild type strain (AP225) to verify the relative attenuation caused by the transposon mutation. Mutant and wild type strains were grown in BHIV¹⁰ to an OD₅₉₀ of 0.6 -- 0.9. Approximately 5.0×10^6 CFU each of the wild type and mutant strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF pig by intratracheal administration with a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lung lavages were performed as described above. Plate counts were carried out on BHIV¹⁰N⁵⁰ and BHIV¹⁰N⁵⁰K¹⁰⁰ to determine the relative numbers of wild type to mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the $[\text{mutant CFU} / \text{wild type CFU}]_{\text{input}} / [\text{mutant CFU} / \text{wild type CFU}]_{\text{recovered}}$.

Of the 35 potential transposon mutants, 22 were significantly attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that did not seem to be attenuated based on the STM screening results was chosen from one of the pools as a positive control. This mutant had a CI in vivo of approximately 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8. The mutant was subsequently determined to contain an insertion between 2 phenylalanine tRNA's.

Competitive indices for unique attenuated single-insertion mutants are listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated that the mutants were unable to compete effectively with the wild type strains and were therefore attenuated.

Table 3
Virulence and Proposed Function of *A. pleuropneumoniae* Mutants

Mutant	Similarity	Putative or Known Functions	C.I.
AP20A6	<i>atpH</i>	ATP synthase	.009
AP7F10	<i>atpG</i>	ATP synthase	.013
AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
AP11E7	<i>exbB</i>	transport of iron compounds	.003, .003, .006
AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
AP13E9	<i>tlg</i>	Peptidyl-prolyl isomerase	.050
AP13C2	<i>flpA</i>	Peptidyl-prolyl isomerase	<.001
AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
AP18F12	<i>hupA</i>	Histone – like protein	.001
AP20F8	<i>dksA</i>	Dosage dependent suppressor of dnaK mutations	.075
AP5G4	<i>dnaK</i>	Heat shock protein – molecular chaperone	.376
AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
AP18B2	<i>rpmF</i>	Protein Synthesis	.112
AP10E7	<i>yaeA</i>	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	<i>apvA</i>	Unknown	.157
AP18F5	<i>apvB</i>	Unknown	.103
AP2A6	<i>apvC</i>	Unknown	.091
AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

Example 10

Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F₁- γ subunit of the F₀F₁ H⁺-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F₁ δ subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al.*, *Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al.*, *J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase. While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et*

al., *Mol Microbiol.* 29:1493-507 (1998), Stojiljkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al.*, *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al.*, *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al.*, *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORFs that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this

appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient
5 folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of
10 *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*, *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J. Bacteriol.* 172:5555-62 (1990), reviewed
15 in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*,
20 *EMBO J.* 14:4939-48 (1995)]. Possible roles include an unknown influence on cell division [Guthrie, and Wickner, *J. Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in
25 *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required
30 for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J*

Bacteriol. 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A.*

pleuropneumonia dnaK mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-glu and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21 (1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same

clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

Example 11

Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 10^{10} CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with 1.5×10^5 CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

Table 4
Efficacy of *A. pleuropneumoniae* Mutants

		% Mortality following intranasal challenge	
<u>Vaccine</u>		<u>Vaccination</u>	<u>Challenge</u>
5	Pleuromune	0	37.5
	exbB	0	0
	tig	12.5	0
	fkpA	12.5	0
	HI0385	50.0	0
10	pnp	0	0
	yaeE	0	0
	atpG	0	0
	None	N/A	50.0

15 The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of 10^{10} CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD₅₀ using this model was generally 1×10^7 CFU, indicating that each of these mutants is at least 100 fold attenuated and that

20 there is a reasonable correlation between CI and attenuation.

Example 12 **Identification of *P. (Mannheimia) haemolytica* Species Homologs**

25 Based on the sequences of virulence genes identified in *P. multocida* and *A. pleuropneumoniae*, attempt were made to identify related genes, i.e., species homologs, in *P. (Mannheimia) haemolytica*. PCR was utilized with the degenerate primers shown below to attempt amplification of the *P. (Mannheimia) haemolytica* genes as indicated. Primer sequences, synthesized by Sigma-Genosys (The Woodlands, TX), include standard single letter designations, wherein B indicates

either (C,G or T), D indicates either (G,A or T), H indicates either (A,C or T), K indicates either (G or T), M indicates either (A or C), N indicates either (A,G,C or T), R indicates either (A or G), S indicates either (G or C), V indicates either (G, A, or C), W indicates either (A or T), and Y indicates either (C or T).

5

atpG	TEF146	ATG GCN GGN GCN AAR GAR AT	SEQ ID NO: 176
	TEF148	GCN GCY TTC ATN GCN ACC AT	SEQ ID NO: 177

10

guaB	TEF240	GGN TTY ATY CAY AAA AAY ATG	SEQ ID NO: 178
	TEF243	TCT TTN GTR ATN GTN ACA TCR TG	SEQ ID NO: 179

pnp	TEF141	GCS GGY AAA CCR CGT TGG GAT TGG	SEQ ID NO: 180
	TEF142	CRC CTA ARA TRT CTG AAA GCA CCA C	SEQ ID NO: 181

15

purF	TEF244	ATG TGY GGN ATY GTN GGN AT	SEQ ID NO: 182
	TEF247	CAT ATC AAT ACC ATA CAC ATT	SEQ ID NO: 183

yjgF	TEF162	GGN CCN TAY GTN CAR G	SEQ ID NO: 184
	TEF163	NGC NAC YTC NAC RCA	SEQ ID NO: 185

20

For amplification of initial degenerate PCR products, a 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers, 0.8 mM MgCl₂, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and approximately 1 µg of TFI DNA.

25

Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 15 s, 40-60°C for 60 s, 72°C for 1.5 min; and a final hold at 72°C for 5 min. Each PCR product was band purified from an agarose gel using the QIAGEN Gel Extraction Kit (QIAGEN, Valencia CA).

30

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for the open reading frame (ORF) for each clone was obtained. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs were used to confirm the identity of the ORF by searching for homologous sequences in currently available databases.

35

The Vectorette Kit (Genosys Biotechnologies, The Woodlands, TX) was used to obtain additional flanking sequence for each of the genes. Vectorette libraries were prepared according to the manufacturer's suggested protocol. Perkin Elmer Applied Biosystems GeneAmp XL PCR Kit components were used to create the

5 Vectorette PCR products with the following reaction conditions. A 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers (shown below), 0.8 mM MgCl₂, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and 1 µl of the appropriate vectorette library. Cycle

10 conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 20 s, 60°C for 45s, 72°C for 4 min; and a final hold of 72°C for 7 min. The second primer for each library was the manufacturer's vectorette primer.

Table 5

Gene	Vectorette library	Primer(s)
5	atpG	BglII, HindIII
		TEF217 GAAGCCGCCATACGCTCTTGGG SEQ ID NO: 186
		ClaI
		TEF218 GTTGCTTCCTTTGCCTGCACTGG SEQ ID NO: 187
10	guaB	EcoRI
		TEF265 GGCTCAGAAACAATACCACITTTCA SEQ ID NO: 188
		HindIII, TaqI
		TEF268 GCACCAAAGCAGAATTGTCC SEQ ID NO: 189
15	pnp	ClaI, HincII
		TEF219 GGTGATGATGTCGATGATAGTCCC SEQ ID NO: 190
		TaqI,
		TEF220 GGCGTATTAGCCGTGATGCCAACC SEQ ID NO: 191
		BamHI
20		TEF286 GACCACTTAGGCGATATGGACTT SEQ ID NO: 192
	purF	TaqI
		TEF271 ACCATCATAAAATCGCCTGATTC SEQ ID NO: 193
		TEF292 ACCTGCGGCATCTTGTCTC SEQ ID NO: 194
25		HincII
		TEF274 ACGGGTTTATTTGCCTCTG SEQ ID NO: 195
	yjgF	ClaI
		TEF221 CGCCGGTTTCAGGATTCACGGG SEQ ID NO: 196
30		EcorV
		TEF281 CTGAACAACGTGAAAGCCAT SEQ ID NO: 197

Vectorette PCR products were band purified and sequenced as described above.

Polynucleotide sequences for the *atpG*, *guaB*, *pnp*, *purF*, and *yjgF* genes are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, respectively. Polypeptides encoded by these genes are set out in SEQ ID NOs: 167, 169, 171, 173, and 175, respectively.

;

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
6. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.

9. The *Pasteurellaceae* bacteria of claim 5 selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

10. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

11. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

12. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in deletion of all or part of said gene.

13. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *P. multocida* bacteria.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *A. pleuropneumoniae* bacteria.

18. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

19. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

20. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in deletion of all or part of said gene.

21. An immunogenic composition comprising the bacteria according to any one of claims 1 through 20.

22. A vaccine composition comprising the immunogenic composition according to claim 21 and a pharmaceutically acceptable carrier.

23. The vaccine composition according to claim 22 further comprising an adjuvant.

24. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

25. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,

31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

26. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174.

27. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

28. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 27,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

29. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109,

111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

30. The polynucleotide of claim 29 which is a DNA.

31. A vector comprising the DNA of claim 30.

32. The vector of claim 31 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

33. A host cell stably transformed or transfected with the DNA of claim 30 in a manner allowing the expression of the encoded polypeptide in said host cell.

34. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 33 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

35. A purified polypeptide produced by the method of claim 34.

36. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

37. An antibody that is specifically reactive with the polypeptide of claim 36.

38. The antibody of claim 33 that is a monoclonal antibody.

39. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 5, 9, or 13 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

40. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

41. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

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Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly	
105 110 115 120	
att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta	617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu	
125 130 135	
ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa	665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys	
140 145 150	
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt	713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe	
155 160 165	
aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca	761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr	
170 175 180	
tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg	809
Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met	
185 190 195 200	
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca	857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala	
205 210 215	
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg	905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp	
220 225 230	
gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg	953
Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
235 240 245	
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac	1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
250 255 260	
taattttttta taaacaaaac cagaccttgg gtctaaattt caatctttatg gagaacatta	1061
tggaacactg taattactac aacaatcatc gcattctgnaa ttntctctgc t	1112

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 <213> *Pasteurella multocida*

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 35 40 45
 Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
 50 55 60
 Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
 65 70 75 80
 His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
 85 90 95
 Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
 100 105 110
 Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
 115 120 125
 Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
 130 135 140
 Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
 145 150 155 160
 Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
 165 170 175
 Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
 180 185 190
 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
 195 200 205
 Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
 210 215 220
 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
 225 230 235 240
 Thr Leu Gln Ala Phe Ile Phe Met Met Leu Thr Val Val Tyr Leu Ser
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 <213> *Pasteurella multocida*

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tatgcgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300
cattttggat agcttcaaag caaacagtcg gtggttaagt aacactttaa atggagagac 360

aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
1 5 10

agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tgc aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
20 25 30

atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
35 40 45

aca ata cgt aac gcg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Thr Ser Lys Ala Thr Ile Gly Tyr
50 55 60

aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
65 70 75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80 85 90 95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
100 105 110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
115 120 125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
130 135 140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
145 150 155

tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160 165 170 175

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att aac acg atg tgc caa aag cca gta ttg gaa aaa tta att cca tta 936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
180 185 190

cca gaa tta gat aat gat gaa tta gcc gaa aga aaa caa gtt tgg gat 984
Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp
195 200 205

tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt 1032
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
210 215 220

cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct 1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala
225 230 235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
240 245 250 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt 1176
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg
260 265 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
275 280 285

gca att taacaaatag aggatcggtat atggcaactg gaaaaattgt acaaatcatc 1280
Ala Ile

ggtgcgggtta ttgacgttga attcccacaa gatgcagttac caaaagtata tgaatgcctta 1340

aatgttgaaa cagggttagt acttgaagtt caacaacaat taggtggtgg tgaagtgcgc 1400

tgtatcgcaa tgggatcatc tgaatggatta aaacgcgggt taagcgtaac aaatacgaat 1460

aaaccaattt ctgttcagtg gggaacgaaa acattgggtc gtatcatgaa cgtattgggt 1520

gaaccaatcg atgagcaagg tgaaatcggt gcagaagaga attggtctat tcaccgtgcg 1580

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<211> 289

<212> PRT

<213> Pasteurella multocida

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Arg Lys Thr	Gln Glu Arg Met Ser	Ser Ser Arg Pro Tyr	Ser Glu Thr
	35	40	45
Ile Arg Asn	Val Ile Ser His	Val Ser Lys Ala Thr	Ile Gly Tyr Lys
	50	55	60
His Pro Phe	Leu Val Asp Arg	Glu Val Lys Lys	Val Gly Met Ile Val
	65	70	75
Val Ser Thr	Asp Arg Gly Leu Cys	Gly Gly Leu Asn	Val Asn Leu Phe
	85	90	95
Lys Thr Val	Leu Asn Glu Met	Lys Glu Trp Lys	Glu Lys Asp Val Ser
	100	105	110
Val Gln Leu	Ser Leu Ile Gly Ser	Lys Ser Ile Asn Phe	Gln Ser
	115	120	125
Leu Gly Ile	Lys Ile Leu Thr	Gln Asp Ser Gly	Ile Gly Asp Thr Pro
	130	135	140
Ser Val Glu	Gln Leu Ile Gly Ser	Val Asn Ser Met	Ile Asp Ala Tyr
	145	150	155
Lys Lys Gly	Glu Val Asp Val	Val Tyr Leu Val	Tyr Asn Lys Phe Ile
	165	170	175
Asn Thr Met	Ser Gln Lys Pro	Val Leu Glu Lys	Leu Ile Pro Leu Pro
	180	185	190
Glu Leu Asp	Asn Asp Glu Leu	Gly Glu Arg Lys	Gln Val Trp Asp Tyr
	195	200	205
Ile Tyr Glu	Pro Asp Ala Lys	Val Leu Leu Asp	Asn Leu Leu Val Arg
	210	215	220
Tyr Leu Glu	Ser Gln Val Tyr	Gln Ala Ala Val	Glu Asn Leu Ala Ser
	225	230	235
Glu Gln Ala	Ala Arg Met Val	Ala Met Lys Ala	Ala Thr Asp Asn Ala
	245	250	255
Gly Asn Leu	Ile Asn Glu Leu	Gln Leu Val Tyr	Asn Lys Ala Arg Gln
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Ala Ser Ile	Thr Asn Glu Leu	Asn Glu Ile Val	Ala Gly Ala Ala Ala
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Ile

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15

gag ttt tat ccg tta gag gca gtg aaa acc aat att tta ggt acg gca 96
 Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala

20

25

30

aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144
 Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys

35

40

45

ctt agc aca gat aaa cgc gtg tac cca att aat gcg atg ggc att tct 192
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser

50

55

60

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa 240
 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu

65

70

75

80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca 288
 Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala

85

90

95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc 336
 Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly

100

105

110

aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca 384
 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr

115

120

125

ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa 432
 Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln

130

135

140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc 480
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr

145

150

155

160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att 528
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile

165

170

175

tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta 576
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu

180

185

190

agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc 624
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg

195

200

205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa 672
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys

210

215

220

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ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act 720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
225                230                235                240

gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa 768
Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
245                250                255

ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta 813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
260                265                270

taaaaaatgaa agtcttagta actggttcaa atggttttat tgcgaaaaat ctgattcagt 873

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cgcttattca tcatgtattg agtgctgatt ggattattca tcttgcgggt gcgaatcgtc 993

cacctgaaga acaagaattt atgacatcaa atacacaatt gacggaaaaa atttgcgcta 1053

ttttacagcg tcatcagaaa aaaacgcctt tgttatattc ctctagcatt caagtagaaa 1113

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<212> PRT
<213> Pasteurella multocida

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20          25          30

Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
35          40          45

Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
50          55          60

Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
65          70          75          80

Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
85          90          95

Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
100         105         110

Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
115         120         125

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Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
 130 135 140
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145 150 155 160
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
 165 170 175
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
 180 185 190
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
 195 200 205
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
 210 215 220
 Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
 225 230 235 240
 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
 245 250 255
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 260 265 270

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 <212> DNA
 <213> *Pasteurella multocida*

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gcatcagggt atttaactta tcgtaaatg attcctgcac tgtataactt atataaaaac 2580

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Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
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gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa 4166
Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
    30                35                40                45

act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
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His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu
65 70 75

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Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile
80 85 90

cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt 4358
Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser
95 100 105

gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa 4406
Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln
110 115 120 125

gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc 4454
Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
130 135 140

tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtg 4502
Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val
145 150 155

atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg 4550
Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
160 165 170

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Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser
175 180 185

agt aaa gcc gag atc tta aaa gaa att caa act act ccg gca gaa caa 4646
Ser Lys Ala Glu Ile Leu Lys Glu Ile Glu Thr Thr Pro Ala Glu Gln
190 195 200 205

ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa 4694
Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu
210 215 220

tgg tat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagattttt 4747
Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
225 230

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<213> Pasteurella multocida

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 35 40 45

Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
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Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr
 65 70 75 80

Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
 85 90 95

Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His
 100 105 110

Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
 115 120 125

Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe
 130 135 140

Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys

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His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile						
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Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala						
	180		185			190
Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr						
	195		200		205	
Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu						
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Asp Lys Asp Ala Ala Lys Leu Leu						
225	230					

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 <222> (1635)..(2396)

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Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
          15          20          25

cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
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ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
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Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
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aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
          80          85          90

cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
          95          100          105

gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
          110          115          120

tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
          125          130          135          140

tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt 2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
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gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150

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Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
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tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat 2198
Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp
      175                      180                      185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc 2246
Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile
      190                      195                      200

gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc 2294
Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Lys Arg Leu Glu Arg
      205                      210                      215

gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca 2342
Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser
      225                      230                      235

tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta 2390
Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu
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Lys Leu

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<213> Pasteurella multocida

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Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu Pro Leu Pro Ile
      20                      25                      30

His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn
      35                      40                      45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln
      50                      55                      60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu
      65                      70                      75                      80

Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile
      85                      90                      95

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu
      100                     105                     110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile
      115                     120                     125

Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
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Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser
      145                     150                     155                     160

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Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
 165 170 175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
 180 185 190

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
 195 200 205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
 210 215 220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln
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<210> 11

<211> 2060

<212> DNA

<213> *Pasteurella multocida*

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<222> (856)..(1389)

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gtcaccagcg agcatgctat tggtaaaagc ttccaggaat ccttaccctt cacagcattg 360

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ggtttgttat ccgccatttc agataatgtg tttgtggcca cagtttatat caatgaaac 540

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attaataacc gtaccaatct tccttctggt gcaaccccaa atggtcacg cgcattctta 660

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atggcattgc cttataccat cgtattatcc tgtattgggt tattgactgt ggaatatatt 780

ttgcctggcg caaccaatgt gctcattcaa attggtttat taaaaccaat gtaatgacaa 840

gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891

Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg

1 5 10

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Ser Ala Trp Phe Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile
      15                20                25

gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
      30                35                40

att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
      45                50                55

ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
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att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
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Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
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gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
      110                115                120

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Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
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ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
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      145                150                155

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Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
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cag cgc aga ctc ttt cat taagtcataa aaaatgggtgc gataaagcac 1419
Gln Arg Arg Leu Phe His
      175

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tcttgctaata aatcttgctt tacgctgctt taagcgtttt aaacgtaatg cgcgtccttg 1539

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<213> Pasteurella multocida

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35 40 45Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
50 55 60Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser
65 70 75 80Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
85 90 95Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
100 105 110Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser
115 120 125Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
130 135 140Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Ala Leu
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Phe His

<210> 13

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<212> DNA

<213> Pasteurella multocida

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<222> (2756)..(3211)

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<223> exbB

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Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
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Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
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Met Asn Lys Asn Arg Tyr
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aaa ctc att ttt agt caa gtc aaa ggt tgt ctc gtt cct gtg gca gaa 1544
Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu
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Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
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Ser Glu Gln Val Glu Glu Pro Phe Leu Leu Glu Gln Tyr Ser Leu
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Ser Ser Val Ser Leu Leu Val Lys Ser Thr Phe Asn Pro Val Ser Tyr
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Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn
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Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr Gln Ala Glu Asn Lys Val
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Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser Ala Val Phe Asn Asn Asn	
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Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu Ile Gly Tyr Ile Pro Gln	
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Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala Asp Val Ile Leu Asn Gln	
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Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu	
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Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu	
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Asn Gly Val Arg Thr Ile Asn Ser Asp Arg Phe Val Ala Thr Thr Ser	
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Glu Leu Ile Asp Pro Asn Gln Met Met Leu Lys Val Thr Lys Gly Asn	
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Val Ile Ile Asp Ile Asp Gly Phe Ser Thr Asp Gly Leu Lys Tyr Leu	
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Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys Lys Ile Thr Ser Gly	
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Asp Asn Ser Glu Ala Lys Thr Asp Val Thr Leu Ile Ala Gly Ser Ser	
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Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn	
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Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Thr Ala Met	
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Lys His Asp Gly Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
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Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
375 380 385 390	

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 Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser
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 Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe
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 Phe Ser Ile Ser Pro Ser Met Leu Ala Ser Leu Ser Ala Gln Phe Lys
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 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
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 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
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 Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
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 Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
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 Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 145 150 155 160
 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 195 200 205
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
 210 215 220
 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
 225 230 235 240
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
 245 250 255
 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
 260 265 270
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
 275 280 285
 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
 290 295 300
 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
 305 310 315 320
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
 325 330 335
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
 340 345 350

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
 355 360 365
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 370 375 380
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 405 410 415
 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
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 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
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 465 470 475 480
 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
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 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 515 520 525
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His Ala Tyr	Gln Asn Gln Pro Leu Ser Thr	Lys Val Val Phe Gln Leu		
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gtg aaa gat	ttg acg gaa gtt tta tac	cgt tct ggc tac	gtg aca agt	144
Val Lys Asp	Leu Thr Glu Val Leu Tyr	Arg Ser Gly Tyr Val Thr Ser		
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gca att ggt	tta aaa aat tca aaa atc	agc aat ggc gat ctt	gaa ttt	192
Ala Ile Gly	Leu Lys Asn Ser Lys Ile Ser	Asn Gly Asp Leu Glu Phe		
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Ile Val Leu	Trp Gly Arg Thr Arg Asp	Leu Phe Val Asn Gly Glu Lys		
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cca acc cgt	ttt aga gat aaa aca atg	tta tca gtc cta ccc	aat tta	288
Pro Thr Arg	Phe Arg Asp Lys Thr Met	Leu Ser Val Leu Pro Asn Leu		
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atc gga aat	cgc tta agt att cac	gac att gac cag ttg	atc gaa atc	336
Ile Gly Asn	Arg Leu Ser Ile His Asp	Ile Asp Gln Leu Ile Glu Ile		
	100	105	110	
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Leu Asn Thr	Thr Asn Lys Lys Ala Thr	Val Asn Val Val Ala Ser Glu		
	115	120	125	
gaa aaa ggc	agc tca aat cta aat att	gaa aga caa tat gat	gtt ttt	432
Glu Lys Gly	Ser Ser Asn Leu Asn Ile	Glu Arg Gln Tyr Asp Val Phe		
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cgc caa gtg	agt gtc gga ttc aat aat	tca ggt gct ggc aat aat	gcc	480
Pro Gln Val	Ser Val Gly Phe Asn Asn Ser	Gly Ala Gly Asn Asn Ala		
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aat ggg cgt	aat caa gct aca ttg aat	att gct tgg agt gat	cta tta	528
Asn Gly Arg	Asn Gln Ala Thr Leu Asn	Ile Ala Trp Ser Asp Leu Leu		
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ggc acg aat	gat cgt tgg agt ttc	tcg agt agt tac cgt	tta tat aaa	576
Gly Thr Asn	Asp Arg Trp Ser Phe Ser	Ser Ser Tyr Arg Leu Tyr Lys		
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aat cat cat	gct aac cag caa cgc	aat tat act ttg tct	tac agt cag	624
Asn His His	Ala Asn Gln Gln Arg Asn Tyr	Thr Leu Ser Tyr Ser Gln		
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Pro Ile Gly	Phe Ser Thr Val Glu Ile	Lys Ala Ser Glu Ser Thr Tyr		
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Glu Lys Glu	Leu Arg Gly Ile Asn Thr His	Ser Ser His Gly Lys Thr		
	225	230	235	240
caa agc tta	gct gtc aag ctg atg cat	gtg tta ttg cgt aat	aag gag	768
Gln Ser Leu	Ala Val Lys Leu Met His	Val Leu Leu Arg Asn Lys Glu		
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agt att tta	tct aca tat acc gag	ttc gag ttt aaa aaa	cgg att agt	816
Ser Ile Leu	Ser Thr Tyr Thr Glu Phe	Glu Phe Lys Lys Arg Ile Ser		
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Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
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Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
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Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
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gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt	1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Ser Gly Ser	
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3247

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<213> Pasteurella multocida

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Glu	Lys	Glu	Leu	Arg	Gly	Ile	Asn	Thr	His	Ser	Ser	His	Gly	Lys	Thr
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Tyr	Phe	Ser	Asp	Ile	Leu	Ile	Gly	Lys	Tyr	His	Asn	Asn	Lys	Val	Ser
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 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
 405 410 415
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
 420 425 430
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
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 Ser Phe

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 <213> *Pasteurella multocida*

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 <222> (639)..(1022)

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 tttcaaatg aaattggtca cttagtacga gtttgcggtg taaggcgggt agcacttttt 240
 gtgtactggc gggtaacata aagggtactgg cttggtgcgc tacaattttt tcattacgat 300
 ttaagttttt agccacaaaa cctaggctgg tcccttcggg taaatgagcg ttgatttcag 360
 caagatcaat ctacgcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
 gttgtaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatata ataattggct 480
 cgagcagttg ctattttttt attgtcgaa aataatagta ttgaaccct cgagagtaaa 540
 tccttttttc gttaaacact tattttttta ttcaactacg gcattgtttt tacaatgttg 600


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Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
      85                      90                      95
Ile Asp Thr Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
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Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
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<212> DNA
<213> Pasteurella multocida

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agcaacgaaa tctgtataat gcgaccgcaa tattttttac ctttttattt ttcataatca 960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
      1                      5                      10
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
      15                      20                      25

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gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro 30 35 40	1108
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile 45 50 55	1156
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser 60 65 70 75	1204
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser 80 85 90	1252
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ggg cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys 255 260 265	1780
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly 270 275 280	1828

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att 1876
 Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile
 285 290 295

ggt cct ggt tca att tgt aca aca cgt att gtc aca gcc gtg ggc gtt 1924
 Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val
 300 305 310 315

cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg 1972
 Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg
 320 325 330

ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att 2020
 Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile
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tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068
 Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met
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cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc 2164
 Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser
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 Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys
 400 405 410

tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta 2260
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 415 420 425

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 Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly
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gtg gcg att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg 2404
 Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val
 460 465 470 475

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc 2450
 Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly
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 <213> *Pasteurella multocida*

<400> 24

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Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
          35             40             45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
          50             55             60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
          65             70             75             80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
          85             90             95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
          100            105            110

Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
          115            120            125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
          130            135            140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
          145            150            155            160

Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
          165            170            175

Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
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Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
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Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
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Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
          225            230            235            240

Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
          245            250            255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
          260            265            270

Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
          275            280            285

Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
          290            295            300

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Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
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 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
 325 330 335
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 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
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 465 470 475 480
 Ala Pro Asn Tyr Arg Met Gly
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<210> 25
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 <213> *Pasteurella multocida*

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 <222> (191)..(1828)

<220>
 <223> H11501

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 aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttggcg 180
 gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
 1 5 10
 gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala 30 35 40 45	325
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala 50 55 60	373
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly 65 70 75	421
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg 80 85 90	469
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val 95 100 105	517
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met 110 115 120 125	565
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gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala 145 150 155	661
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asn Leu Leu Leu 160 165 170	709
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290 300	
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320 325 330	
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350 355 360 365	
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370 375 380	
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385 390 395	
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400 405 410	
gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp	1477
415 420 425	
tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln	1525
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465 470 475	
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480 485 490	
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495 500 505	
gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His	1765
510 515 520 525	
gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu	1813
530 535 540	

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 Gly Gly Thr Asn Val
 545

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 aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048
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<210> 26

<211> 545

<212> PRT

<213> Pasteurella multocida

<400> 26

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Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys
 35 40 45

Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu
 50 55 60

Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile
 65 70 75 80

Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu
 85 90 95

Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
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Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met
 115 120 125

Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys
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Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln
 145 150 155 160

Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro
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Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His
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 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr
 225 230 235 240
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu
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 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn
 260 265 270
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn
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 305 310 315 320
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 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
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 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
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 385 390 395 400
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 405 410 415
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
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 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
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 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
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 465 470 475 480
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys
 485 490 495
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala
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Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
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Asn Val
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Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
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Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
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cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
50 55 60
gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys	85 90 95
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Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr	100 105 110
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Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe	115 120 125
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Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe	130 135 140
cgg cgg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	145 150 155 160
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	165 170 175
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Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg	180 185 190
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Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Ser His Asn Ile	195 200 205
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Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	210 215 220
tat caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca	721
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala	225 230 235 240
tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat	769
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	245 250 255
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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	260 265 270
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Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	275 280 285
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Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	290 295 300
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	305 310 315 320
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Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His	325 330 335

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 370 375 380
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 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
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 50 55 60
 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
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 Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
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 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
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 Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
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 Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
 145 150 155 160
 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
 165 170 175
 Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
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 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
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 Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
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 340 345 350

Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
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 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
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 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
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Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
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gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
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Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
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Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala
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Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly
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 165 170 175
 Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr
 180 185 190
 Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln
 195 200 205
 Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu
 210 215 220
 Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg
 225 230 235 240
 Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys
 245 250 255
 Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp
 260 265 270
 Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val
 275 280 285
 Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn
 290 295 300

Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr
 305 310 315 320
 Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
 325 330 335
 Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu
 340 345 350
 Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
 355 360 365
 Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu
 370 375 380
 Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr
 385 390 395 400
 Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr
 405 410 415
 Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
 420 425 430
 Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
 435 440 445
 Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
 450 455 460
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
 465 470 475 480
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
 485 490 495
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
 500 505 510
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 515 520 525
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 530 535 540
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 Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
 565 570 575
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
 580 585 590
 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
 595 600 605
 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
 610 615 620
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
 625 630 635 640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
 645 650 655
 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
 660 665 670
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
 675 680 685
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
 690 695 700
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
 705 710 715 720
 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
 725 730 735
 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
 740 745 750
 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
 755 760 765
 Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
 770 775 780
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
 785 790 795 800
 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
 805 810 815
 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
 820 825 830
 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
 835 840 845
 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
 850 855 860
 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
 865 870 875 880
 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
 885 890 895
 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
 900 905 910
 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
 915 920 925
 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
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 945 950 955 960
 Leu Ser Ala Glu Ile Thr Phe
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ttcttcgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaacac 180
gtctaaagt gcggtctgtt ttgscgcat ttctaattca aataaggtat catggcgcgc 240
aaccatgatc attttgacac catgatgttc acctaactta tcttcgccta accacagttc 300
tgccccctct ttcggtgctt ttgaggagcg cacatgggct aaaaagcgtg tgcgggataa 360
aatccgctcg accaacactt ccaccttacc gccactggct ttacgtccaa acatccttgc 420
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atcagcaaaa gtgcggtggg taatctcacc attttgcgcg ttaagttgta ataacgcgact 540
agcgggtcga tccggttttg ggtaacgagc aatcagctca tcgggtaaat caaaaaataa 600
gtcagaaaca cgcataaata ggggtataaa aagttatcta aaaaatcgtg ggcgtaagtc 660
tagtgtgaat tccgctcttg cacaaggaaa aatccagatt ttgttgttta gtatcgaatt 720
gagatgattt tggacaaaaa aaaagccctt tcaagaaaaga cgaaggggcg aaaatatatt 780
tggagtcata ctttttaggg tatgtgtcgg attatacaca aaaaaataac aaatgcaaca 840
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ctaaaggatg atttatttag cctattaaaa aaacacatga gatgagagtt tgcgagagcg 960
gtaataaaag tgcggtgggt tttagaaaag ttttgaatag gatcacaaat taaccaaagt 1020
tttgtaaata ccaagtagta gtttttaagt atatgatgaa tcatatgcta aagtttaaac 1080
ccgttaaata accaagaggt ggaag atg aca gaa aat aaa gga aag aga 1132
Met Thr Glu Glu Asn Lys Gly Lys Arg
1 5

tat ttt tta tgg ttc ata ttg ttt atc ctt tca atc tat tta ttt att 1180
Tyr Phe Leu Trp Phe Ile Leu Phe Ile Leu Ser Ile Tyr Leu Phe Ile
10 15 20 25

acc ata caa gaa aga cga ggt tat tgt ttt gac aaa cgt gca tat att 1228
Thr Ile Gln Glu Arg Arg Gly Tyr Cys Phe Asp Lys Arg Ala Tyr Ile
30 35 40

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cat gag ctt tat act gag caa gag tta att gat cgg ggg att gaa tat 1276
His Glu Leu Tyr Thr Glu Gln Glu Leu Ile Asp Arg Gly Ile Glu Tyr
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gtg gta tcc acc atg ccg tca ggt gtt att aaa cca gat ggc aca ata 1324
Val Val Ser Thr Met Pro Ser Gly Val Ile Lys Pro Asp Gly Thr Ile
60 65 70
aaa gaa gta aag cgt tac acg agt gtc gag gag ttt aaa cag atg aac 1372
Lys Glu Val Lys Arg Tyr Thr Ser Val Glu Glu Phe Lys Gln Met Asn
75 80 85
cca gct tgt tgt aca tta acc acc ttt att gat gaa gga ggc gat ggc 1420
Pro Ala Cys Cys Thr Leu Thr Thr Phe Ile Asp Glu Gly Gly Asp Gly
90 95 100 105
tat cca gat gat gat gga tat ggt tat gtc aga att gaa tat tta aga 1468
Tyr Pro Asp Asp Asp Gly Tyr Gly Tyr Val Arg Ile Glu Tyr Leu Arg
110 115 120
cat tat gtt gag aat cta aaa cct tat cat aga gtg att tat ctt gaa 1516
His Tyr Val Glu Asn Leu Lys Pro Tyr His Arg Val Ile Tyr Leu Glu
125 130 135
tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564
Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn
140 145 150
taagagttag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624
tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684
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 ggcgtattct ggacgttggt tattatcagg ctatattaat aaacgtgac caaatcaagg 2824
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 cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaag aatgtgacac cgacacttgg 2944
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 Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
 35 40 45
 Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
 50 55 60
 Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
 65 70 75 80
 Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
 85 90 95
 Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
 100 105 110
 Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys
 115 120 125
 Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu
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 Arg Glu Glu Ala Ala Phe Ser Lys Asn
 145 150

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gcagaactgg ctacttctac acttttagat aattgtatta ttaaaagaag ctgtatgatt 180
gttattctat cattagtggg taataaatat tctttatatt ttgagagata aaaacaattc 240
atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300
tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351
                               Met Asn Ile Leu Phe Val Ser Asp Asp
                               1           5

ggt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
10           15           20           25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
30           35           40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa 495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
45           50           55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt 543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
60           65           70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca 591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
75           80           85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
90           95           100           105

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gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat 687
 Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn
 110 115 120

aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag 735
 Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys
 125 130 135

tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt 783
 Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe
 140 145 150

aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat 831
 Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp
 155 160 165

gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg 879
 Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Glu Met
 170 175 180 185

att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc 927
 Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val
 190 195 200

tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga 975
 Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg
 205 210 215

ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa 1023
 Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu
 220 225 230

aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa 1071
 Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys
 235 240 245

gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa 1119
 Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys
 250 255 260 265

ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct 1167
 Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser
 270 275 280

ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc 1215
 Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe
 285 290 295

aaa tat caa gtc tat taactattga atttttgc aa atgagataag agtatagtgc 1270
 Lys Tyr Gln Val Tyr
 300

tgattttctc aaagcgaaaa ggaggaaata gcttgttcta atttattaca ataattggtg 1330

tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttctgcacct 1390

aaatttacta atctctccaaa ttctctctct cgnagaattt ctttcggacc ggtatggcag 1450

tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc 1510

tctttcaaa aggtgtgtaa aaatagctta gcatttttta ttaattggata cggattatct 1570

ttattttcta aaagaaaaa atcttcttgt agattgagtg attctatttg ttctctaat 1630

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 35 40 45
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140

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Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145                      150                      155                      160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                      165                      170                      175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
                      180                      185                      190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
                      195                      200                      205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
210                      215                      220

Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225                      230                      235                      240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
                      245                      250                      255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
                      260                      265                      270

Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
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Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
290                      295                      300

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gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
      20             25             30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
      35             40             45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
      50             55             60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
Ser Lys Ala Asn Gln Ile Glu Val Ile Ala Asn Asn Asp Gly Met
      65             70             75             80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
      85             90             95

atc ttc ngt gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
      100            105            110

ggg gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
      115            120            125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
      130            135            140

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gaa ggc aca aaa tgg cag tta aaa cga tgg tgt cct acg tat ccc tta 481
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Cys Trp Cys Gly Cys Gly
          165

tataacaaaa caagamtgtg taattctcgg ggagggtatc cctccccctt tttatgtgag 589
gttggatatg acaactcaaa ttccaaatca agacagttaa atactgctca caatgaccaa 649
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tcctcgcttt cagaaaaaga agttgaacac ctatttaaaa ttatcgcgaa gctaaaaaaa 1189
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gtatcgacat tgggtcgaaa tatgaaattt atcagctgat tatggagtta gcaaaaaaag 1969
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<212> PRT
<213> Pasteurella multocida

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Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
          35           40           45

Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
          50           55           60

Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
          65           70           75           80

Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
          85           90           95

Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
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Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
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Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
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Cys Trp Cys Gly Cys Gly
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Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
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Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
45 50 55
cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
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Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
75 80 85
ggg tta ggt aat tcg gat tat gat acc ttc tgt cac gca gtg gat cat 640
Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
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gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
Val Glu Gln Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
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<212> PRT

<213> Pasteurella multocida

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Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
 35             40             45

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Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile
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Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile
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cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
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Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val
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Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
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Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu
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Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
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acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
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tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat 3808

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Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr
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 Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg
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 atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc 3904
 Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val
 220 225 230
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 Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg
 235 240 245 250
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 255 260 265
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 Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln
 270 275 280
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 Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile
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<213> Pasteurella multocida

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 35 40 45

Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu
 50 55 60

Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
 65 70 75 80

Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile
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Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu
 100 105 110

Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys
 115 120 125

Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu
 130 135 140

Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr
 145 150 155 160

Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val
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Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
 180 185 190

Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly
 195 200 205

Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly
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Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
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Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser

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Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg			
20	25	30	
atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct			144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala			
35	40	45	
gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc			192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile			
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agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc			240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile			
65	70	75	80
gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca			288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr			
85	90	95	
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Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg			
100	105	110	
aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct			384

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Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu	
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aca	ggg	gag	cgt	tca	gat	cac	ttc	tta	ttc	cac	tac	aac	ttc	ccg	cca	480
Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro	
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Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu	
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Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro	
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Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr	
	195					200						205				
gaa	tca	aat	ggg	tct	tct	tct	atg	gca	tcg	gtt	tgt	ggg	gcg	tct	tta	672
Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu	
	210					215					220					
gca	tta	atg	gat	gcg	ggg	gta	cca	att	aaa	gcg	gcg	gtt	gca	ggg	att	720
Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile	
	225				230				235					240		
gca	atg	ggc	tta	gtc	aaa	gaa	gac	gaa	aaa	ttt	gtg	gtg	ctt	tca	gac	768
Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp	
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Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala	
		260						265					270			
ggg	aca	cgt	acg	ggg	gtg	acg	gca	tta	caa	atg	gat	atc	aaa	atc	gaa	864
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu	
		275					280					285				
ggg	atc	aca	gca	gaa	atc	atg	caa	att	gcg	tta	aac	caa	gcg	aaa	agc	912
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser	
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gca	cgt	tta	cac	att	tta	ggg	gtg	atg	gag	caa	gcg	atc	cca	gcg	cca	960
Ala	Arg	Leu	His	Ile	Leu	Gly	Val	Met	Glu	Gln	Ala	Ile	Pro	Ala	Pro	
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cgt	gcg	gat	att	tct	gat	ttt	gca	ccg	cgt	att	tac	act	atg	aaa	att	1008
Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	Arg	Ile	Tyr	Thr	Met	Lys	Ile	
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gat	ccg	aag	aaa	atc	aaa	gat	gtg	atc	ggg	aaa	ggg	ggg	gca	acc	att	1056
Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	Gly	Lys	Gly	Gly	Ala	Thr	Ile	
		340						345					350			
cgt	gcc	tta	aca	gaa	gaa	aca	ggg	acc	tca	att	gat	atc	gat	gat	gat	1104
Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp	
		355					360						365			

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Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct 1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa 1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg 1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

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Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
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Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat 1494
Asp Val Ala Ala Glu Glu Asn Ala
485

aaagggcggtt ggtgtgcatg ttgataagta caatttgtgc ttttaaggcga agcgaaatga 1554

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<213> Pasteurella multocida
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 35 40 45
 Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
 50 55 60
 Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
 65 70 75 80
 Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
 85 90 95
 Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
 100 105 110
 Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
 115 120 125
 Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
 130 135 140
 Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
 145 150 155 160
 Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
 165 170 175
 Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
 180 185 190
 Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
 195 200 205
 Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
 210 215 220
 Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
 225 230 235 240
 Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
 245 250 255
 Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
 260 265 270
 Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
 275 280 285
 Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
 290 295 300
 Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
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 Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
 325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
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 Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
 355 360 365
 Gly Thr Val Lys Ile Ala Val Asp Gly Asn Ser Ala Lys Glu Val
 370 375 380
 Met Ala Arg Ile Glu Asp Ile Thr A^a Glu Val Glu Ala Gly Ala Val
 385 390 395 400
 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
 405 410 415
 Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
 420 425 430
 Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
 435 440 445
 Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
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 Asp Val Ala Ala Glu Glu Asn Ala
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 <212> DNA
 <213> Pasteurella multocida

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 <222> (2)..(631)

<220>
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 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
 20 25 30
 gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
 35 40 45
 cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
 50 55 60
 gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65 70 75 80

ggt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn 95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln 100 105 110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala 115 120 125

tct gct gca cca gaa att cgt tat ggt ggt att gat atg 433
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met 130 135 140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481
Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile 145 150 155 160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg 529
Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala 165 170 175

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Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp 180 185 190

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Tyr Leu 210

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<213> Pasteurella multocida

<400> 46

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20 25 30

Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala 45
35 40 45

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr 60
50 55 60

Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser 80
65 70 75 80

Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn 95
85 90 95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln 110
100 105 110

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Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
    115                      120                      125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
    130                      135                      140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
    145                      150                      155                      160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
    165                      170                      175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
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Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
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Tyr Leu
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<210> 47
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att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata 96
Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
    20                      25                      30

act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta 144
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
    35                      40                      45

aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat 192
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
    50                      55                      60

ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc 240
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
    65                      70                      75                      80

gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata 288
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
    85                      90                      95

aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa 336

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Pro	Lys	Asn	Ser	Ala	Glu	Arg	Lys	Glu	Arg	Tyr	Ser	Glu	Gln	Asp	Ile	
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aaa	aca	ata	tta	gaa	aca	gct	aga	tat	tgt	gaa	gat	aaa	cta	ccc	ata	432
Lys	Thr	Ile	Leu	Glu	Thr	Ala	Arg	Tyr	Cys	Glu	Asp	Lys	Leu	Pro	Ile	
		130					135				140					
aca	ctc	aaa	caa	aga	gta	gca	att	gca	atg	tta	ttt	gct	att	gaa	acc	480
Thr	Leu	Lys	Gln	Arg	Val	Ala	Ile	Ala	Met	Leu	Phe	Ala	Ile	Glu	Thr	
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gct	atg	cgt	gct	ggc	gag	att	gct	agt	ata	aaa	tgg	gat	aat	gtt	ttt	528
Ala	Met	Arg	Ala	Gly	Glu	Ile	Ala	Ser	Ile	Lys	Trp	Asp	Asn	Val	Phe	
				165					170					175		
ctt	gaa	aag	aga	ata	gta	cat	tta	ccg	aca	act	aaa	aac	ggg	cac	tct	576
Leu	Glu	Lys	Arg	Ile	Val	His	Leu	Pro	Thr	Thr	Lys	Asn	Gly	His	Ser	
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Arg	Asp	Val	Pro	Leu	Ser	Gln	Arg	Ala	Val	Ala	Leu	Ile	Leu	Lys	Met	
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Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln	Thr	Thr	Pro	Glu	Ser	
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Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu	Cys	Gly	Leu	Glu	His	
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Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu	Thr	Arg	Leu	Ser	Lys	
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Lys	Val	Asp	Val	Met	Thr	Leu	Ala	Lys	Ile	Ser	Gly	His	Arg	Asp	Leu	
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Asn	Leu	Leu	Asp													
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<210> 48

<211> 292

<212> PRT

<213> Pasteurella multocida

<400> 48

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Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
  1                   5                   10                   15

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Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
      20                      25                      30
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
      35                      40                      45
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
      50                      55                      60
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
      65                      70                      75                      80
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
      85                      90                      95
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
      100                     105                     110
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
      115                     120                     125
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
      130                     135                     140
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
      145                     150                     155                     160
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
      165                     170                     175
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
      180                     185                     190
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
      195                     200                     205
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
      210                     215                     220
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
      225                     230                     235                     240
Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
      245                     250                     255
Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
      260                     265                     270
Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
      275                     280                     285
Asn Leu Leu Asp
      290

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<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(1195)

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<220>

<223> sopE

<400> 49

g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49
 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile

1

5

10

15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly

20

25

30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn

35

40

45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly

50

55

60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val

65

70

80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp

85

90

95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile

100

105

110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys

115

120

125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp

130

135

140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn

145

150

155

160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala

165

170

175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met

180

185

190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp

195

200

205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa 673
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu

210

215

220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser

225

230

235

240

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ggg gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat 769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
245 250 255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat 817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
260 265 270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc 865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
275 280 285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att 913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

gca ggg cgc ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

gtg aaa gat att att gaa gca atc aat cgc aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

aca aaa ggc tac tta att ggc ggt aaa cgc tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

aac agt gca acg aat tta aaa gat cgc aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

taagggggat aaaatggcctt taccacgcaa acttaaatgt atgaatttaa tcatcgacgg 1255

taacaaatat ctgcgggaag tcacggaagt gactcaacca aaattagcaa tgaaaaatcga 1315

agaatttcgc gcggcggtta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaat tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcgggtc 1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctgtt gagcttgtga tgcaaggctcg atttactgaa attgacagcg gaaacagcaa 1555

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tga 1618

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<210> 50

<211> 398

<212> PRT

<213> Pasteurella multocida

<400> 50

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 20 25 30
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
 35 40 45
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
 50 55 60
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
 65 70 75 80
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
 85 90 95
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
 100 105 110
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
 115 120 125
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
 130 135 140
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
 145 150 155 160
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
 165 170 175
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
 180 185 190
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
 195 200 205
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
 210 215 220
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
 225 230 235 240
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
 245 250 255
 Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
 260 265 270
 Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
 275 280 285
 Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
 290 295 300
 Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
 305 310 315 320
 Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
 325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
 340 345 350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
 355 360 365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
 370 375 380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 51
 <211> 353
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(351)

<220>
 <223> unknown C1

<400> 51
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 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52
 <211> 117
 <212> PRT
 <213> Pasteurella multocida

<400> 52
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110
 Val Ile Tyr Lys Arg
 115

<210> 53
 <211> 509
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(507)

<220>
 <223> unknown C2

<400> 53
 atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
 Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15
 gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
 20 25 30
 cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
 Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
 35 40 45
 gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192
 Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
 50 55 60
 tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240
 Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
 65 70 75 80
 ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288
 Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
 85 90 95

tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336
 Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
 100 105 110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384
 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
 115 120 125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
 130 135 140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
 145 150 155 160

ttt gat gaa atg ata gag aag tat tcg ta 509
 Phe Asp Glu Met Ile Glu Lys Tyr Ser
 165

<210> 54

<211> 169

<212> PRT

<213> Pasteurella multocida

<400> 54

Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
 20 25 30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
 35 40 45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
 50 55 60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
 65 70 75 80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
 85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
 100 105 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
 115 120 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
 130 135 140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
 145 150 155 160

Phe Asp Glu Met Ile Glu Lys Tyr Ser
 165

<210> 55

<211> 443

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(441)

<220>

<223> unknown C3

<400> 55

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Met	Ile	Lys	Tyr	Leu	Glu	Gly	Asn	Ile	Asn	Ser	Phe	Ile	Ser	Ala	Leu	
1				5					10					15		

ggc	aaa	aac	gaa	agt	aat	aaa	gat	att	tta	aaa	tta	gta	gaa	ata	gtt	96
Gly	Lys	Asn	Glu	Ser	Asn	Lys	Asp	Ile	Leu	Lys	Leu	Val	Glu	Ile	Val	
			20					25					30			

tct	tca	gat	ttt	gaa	gtg	gat	gaa	cta	agt	cat	aaa	gat	gaa	cac	gag	144
Ser	Ser	Asp	Phe	Glu	Val	Asp	Glu	Leu	Ser	His	Lys	Asp	Glu	His	Glu	
		35					40					45				

ata	tat	tat	ttg	ttt	tat	aag	agg	ggc	gtt	gaa	ttt	tgt	ttt	aaa	aga	192
Ile	Tyr	Tyr	Leu	Phe	Tyr	Lys	Arg	Gly	Val	Glu	Phe	Cys	Phe	Lys	Arg	
	50					55					60					

ata	gat	gaa	gag	tat	gtc	tta	tat	tcg	gtt	ttc	ttt	ttc	ttg	gta	gag	240
Ile	Asp	Glu	Glu	Tyr	Val	Leu	Tyr	Ser	Val	Phe	Phe	Phe	Leu	Val	Glu	
	65				70					75				80		

gtt	gat	aat	tat	ttt	tca	tgc	cca	ttt	att	cat	gaa	tta	ata	tgt	gat	288
Val	Asp	Asn	Tyr		Phe	Ser	Cys	Pro	Phe	Ile	His	Glu	Leu	Ile	Cys	
			85						90					95		

ctt	aaa	cac	gga	ttc	tca	ata	gag	gat	att	ata	agg	ttt	tta	ggg	gag	336
Leu	Lys	His	Gly	Phe	Ser	Ile	Glu	Asp	Ile	Ile	Arg	Phe	Leu	Gly	Glu	
			100					105					110			

cca	aat	ttt	aaa	ggc	agt	ggc	tgg	gta	aga	tat	tct	tat	aat	gga	aga	384
Pro	Asn	Phe	Lys	Gly	Ser	Gly	Trp	Val	Arg	Tyr	Ser	Tyr	Asn	Gly	Arg	
		115					120					125				

aat	att	cat	ttc	gaa	ttt	aat	gaa	tct	aat	gaa	tta	tcc	cag	att	agc	432
Asn	Ile	His	Phe	Glu	Phe	Asn	Glu	Ser	Asn	Glu	Leu	Ser	Gln	Ile	Ser	
	130					135					140					

att	ttt	att	ta													443
Ile	Phe	Ile														
145																

<210> 56

<211> 147

<212> PRT

<213> Pasteurella multocida

<400> 56

Met	Ile	Lys	Tyr	Leu	Glu	Gly	Asn	Ile	Asn	Ser	Phe	Ile	Ser	Ala	Leu
1				5					10					15	

Gly	Lys	Asn	Glu	Ser	Asn	Lys	Asp	Ile	Leu	Lys	Leu	Val	Glu	Ile	Val
		20						25					30		

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Leu Val Glu
 65 70 75 80
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125
 Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 130 135 140
 Ile Phe Ile
 145

<210> 57
 <211> 8498
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> unknown C

<400> 57
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 aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcctttc 180
 tttgctggcg atattcagca agtcgctcat ctgcgaaag ccgcagaaat ggggtgcgtg 240
 gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggt gataccggga 300
 gtaaatcagg aaaaattggt agatttacgt cagcgtaata ttgtgtcctt agcgcagcca 360
 caagtgcac aacttgcat agtcacgccc tcgttgatgt caaatcacga aatcaaagac 420
 attgccgtaa cctcgattat acctgcatct tatactaacg gagaaacggt aggtaaatta 480
 gcgggacaaa cagcgcgatt gttaaatggc attccacttg atgaaggcga acaacgttta 540
 gcttttgatg ttttccctac gcctgcatcg catttaaata tgcaaatca caagatcttt 600
 ccacaattag ataattgctg atttcattct atccaagtgc ctgttttcta cgggatgggg 660
 caaatggtga gcgattatgc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720
 actgacaatc cgttgatgac ttatcatgca gaaaaatatt gacccccagt gacgaatggc 780
 gaacaggaaa tggcagaaga gcaagcagca aaattacata taagtggggt aagtgcggtg 840
 gaaaatggtc tacaattttg gtcggttgca gatgaacagc gctttaatct tgctttattg 900

agtgttacgc ttgcagagtt aatttactcg caagggttatt aattttaaag tgtttttgca 960
cgatattttt atcttgaact ttgagagcgc actcgttttt gacgagtgcg tttttgttaa 1020
aacattcggt tgaaagacag tgaatgaata gcggagttat tgataagaat caattttatac 1080
aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagtttt agttggcgcc 1140
ataatacata aactgtactt aataatatgc aatcaatacc tagaataatt catgacgtaa 1200
tccaacatat cggggagggg attttaagtg atggtagaaa aaacatttag aaactctaaa 1260
atatatgatg attatggttc tgtctctcag gaaattattt ttaattttga aaaagagttt 1320
gatataaaac tccctttatc ctatatctca cttgtgaaaa agtataatgg cgtttggttt 1380
aaggaaagtg attttgataa tttatctcaa aatgggaaaa gaataataag ctcattgagt 1440
tttgatagtt ttgagacaaa agataatgc gaaccaatga ataatatatt aagacaatat 1500
atttatgatg atgaaattta tggatataag aatgtttatt cttttgggta cactggaaat 1560
ggtgactttg tctgttttga ttatcgtgat gaccctaaag gtgatgagcc caaatctgt 1620
atcgtgatcc atgatgaata tgatgaaaaa acaggcaagc gtttgttatt gcctgtggca 1680
gaaaattttg aggcattttt agatatgctt tacgattttg atgaacgcta tccgaatggt 1740
tatgaatagg tatttgttta aataatgtgt tgtatttttt aagcattatt tacaactaac 1800
attttaagtg cggccaattt tgaaaaggt ttgggctttg agaattgggc gcattttttt 1860
tgaaatattc ttcaatgatg agcactaatt atggattaga taatgggaat tatcgagata 1920
tggatggtaa taaaggatgg aggctagatt ttgatcctga gaaagtgttt catgtaaata 1980
tttttgactt tactaaaggt aaaggactag gtaaagcagt taaaaagtca ttttttttga 2040
tagtactgaa caagagtttg aaaaatttta aagcaattaa ataaggaaga taaaatgaca 2100
ttatttgatg aatgtaaat agctcttaga gacgatttta atctaatttg tgatgaagag 2160
aaggattgtg taatggataa gttttatttc tattttttgg aaaagaaaga ggaatttaat 2220
tttcaagatt attcatttga agaaatgtat atattttcaa aaatggaaac tgtgtatggt 2280
ttatgtgata gctctaatat acccttggtt aggagtaatt ggggaattgat tatcaataat 2340
atatatgatg ttgtctgttt atctacaaaa gtattttttc tagatgatga aaagttaatg 2400
atggaattat ttcctgaaga taaagtaaga gtcactata aaagataaatt accccttgat 2460
cgcgctcggt tcagcacgag ttcgctttca ttaaagctct cgtaaagac tagcactagc 2520
agtgagggtg atcgtaatca atttactgaa gaacagttaa ttaaaattaa taagaggctt 2580
gataaaatag agggattttc atggcatcat aactcacaaa gtatgcccc aaatatgtag 2640
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<211> 587

<212> PRT

<213> *Pasteurella multocida*

<400> 59

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 20 25 30

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 35 40 45

Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala

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Gly Asp Val Asn Arg Gln Val Val Ser Pro Gln Asp Lys Ala Lys Phe		
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Gly Gly Asn Glu Phe Met Ala Lys Gln Glu Lys Arg Asn Gln Glu Leu		
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Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala		
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Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys		
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Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro		
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Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro		
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Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val		
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Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val		
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Ile Pro Val Glu Leu Met Leu Val Ser Asp Tyr Ser Gly Ser Met Asn		
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Ser His Leu Gln Asp Lys Asn Gly Arg Ser Leu Gly Lys Ala Lys Ile		
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Thr Ile Leu Arg Glu Val Val Ser Glu Ile Ser Lys Ile Leu Leu Pro		
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Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr		
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Thr Phe Ser Gly Gly Val Arg Gln Arg Asp Val Thr Glu Gly Cys Val		
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Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile		
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Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly		
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Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr		
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Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg		
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Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu		
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Lys Ile Asn Asp Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile		
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Asp Val Ser Gly Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn		

385 390 395 400
 Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly
 405 410 415
 Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys
 420 425 430
 Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser
 435 440 445
 Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn
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 Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg
 465 470 475 480
 Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser
 485 490 495
 Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu
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 Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg
 515 520 525
 Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala
 530 535 540
 Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
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 Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe
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 <213> Pasteurella multocida

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Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Gly Cys Ser
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acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
25 30 35
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<210> 61

<211> 257

<212> PRT

<213> Pasteurella multocida

<400> 61

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Ser	Met	Ser	Ser	Glu	Thr	Ile	Thr	Ala	Lys	Glu	Thr	Leu	Tyr	Glu	Ser
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Thr	Gln	Asn	Tyr	Ser	Ala	Leu	Ile	Ser	Leu	Tyr	Arg	Asp	Val	Leu	Lys
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Ala	Lys	Glu	Asp	Pro	Ser	Ile	Arg	Tyr	Lys	Leu	Ala	Lys	Thr	Tyr	Tyr
		65				70				75				80	
Gln	Arg	Gly	Asp	Ser	Lys	Ser	Ser	Leu	Leu	Tyr	Leu	Thr	Pro	Leu	Leu
			85					90						95	
Asn	Asp	Asn	Thr	Lys	Leu	Ala	Thr	Gln	Ala	Lys	Ile	Leu	Gln	Ile	Lys
			100					105					110		
Asn	Leu	Ile	Gln	Leu	Asn	Asn	Phe	Gln	Glu	Ala	Ile	Ser	Val	Ala	Asn
			115					120				125			

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 Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp
 145 150 155 160
 Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn
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 Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val
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 Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu
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 Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr
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Arg

<210> 62

<211> 1788

<212> DNA

<213> *Pasteurella multocida*

<220>

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<222> (1)..(600)

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<400> 62

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 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
 20 25 30
 aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45
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 65 70 75 80
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Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn	115	120	125	
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Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys	130	135	140	
ggt gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc				480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu	145	150	155	160
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat				528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr	165	170	175	
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Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr	180	185	190	
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Glu Leu Asn Val Asp Arg Val Ser	195	200		
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 <212> PRT
 <213> *Pasteurella multocida*

<400> 63
 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
 1 5 10 15
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
 20 25 30
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
 50 55 60
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65 70 75 80
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
 85 90 95
 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
 100 105 110
 Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
 115 120 125
 Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
 130 135 140
 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
 145 150 155 160
 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
 165 170 175
 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
 180 185 190
 Glu Leu Asn Val Asp Arg Val Ser
 195 200

<210> 64
 <211> 278
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <221> CDS
 <222> (108)..(278)
 <220>

<223> unknown O

<400> 64

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cattaccccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
                                     Met Lys Ile
                                     1
act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
      5                10                15
gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
      20                25                30                35
gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
                40                45                50
agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
                55

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<210> 65

<211> 57

<212> PRT

<213> Pasteurella multocida

<400> 65

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Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
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Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
                20                25                30
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
                35                40                45
Glu Glu Glu Ser Lys Arg Gly His Ser
      50                55

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<210> 66

<211> 1020

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(597)

<220>

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<400> 66

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Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
      1                5                10                15
gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
20 25 30
tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
35 40 45
ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
50 55 60
ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65 70 75 80
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
85 90 95
act gca caa atc tta aaa gat acg att gca ggg cgc ttt gat tgg gca 336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
100 105 110
gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
115 120 125
atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
130 135 140
ggc aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145 150 155 160
gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
165 170 175
gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
180 185 190
ttt tca aat cgt tta gca tcg taagggttag aaaatggcctt taccacgcaa 627
Phe Ser Asn Arg Leu Ala Ser
195
acttaaatgt atgaatttaa tcatcgacgg taacaaatat ctgcgcgaag tcacggaagt 687
gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcggcgcggtg tgattggctc 747
gggtgatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807
ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867
ctcatatcag cgtgatgaca cagaagaagt cacatctggt gagcttgta tgcaaggtcg 927
atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987
agtgccttta acgtattaca aaatcattgt tga 1020

<210> 67

<211> 199

<212> PRT

<213> Pasteurella multocida

<400> 67

Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gly Trp His Thr Ser Ile
 20 25 30

Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 50 55 60

Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80

Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95

Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110

Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125

Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140

Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160

Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175

Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190

Phe Ser Asn Arg Leu Ala Ser
 195

<210> 68

<211> 2584

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1042)..(2286)

<220>

<223> xylA

<400> 68

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 taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120
 cgcgatggtc tttttgggtc ttatttacgt gctgttttagc agtattgtgg catttaaaat 180

tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala 140 145 150	1503
gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Ala Gln Val 155 160 165 170	1551
ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val 175 180 185	1599
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu 190 195 200	1647
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu 205 210 215	1695
cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys 220 225 230	1743
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val 235 240 245 250	1791
tat ggc ttt tta aag cag ttt ggt tta gaa gaa att aaa gtg aat Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn 255 260 265	1839
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Gly 270 275 280	1887
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn 285 290 295	1935
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser 300 305 310	1983
gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gln 315 320 325 330	2031
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser 335 340 345	2079
acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val 350 355 360	2127
ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala 365 370 375	2175
tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu 380 385 390	2223

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ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
395 400 405 410

cta aca aaa gtg ctt taaaacgttc cggttacgc cagacatcta gacgattgaa 2326
Leu Thr Lys Val Leu
415

taattttcaat attgtctcgc cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386

acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgc gacataagcg 2446

tcttgcgcgc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506

tgtaaggct tttcctaata catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566

gtcgtgtttt tctgtcga 2584

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<210> 69
<211> 415
<212> PRT
<213> Pasteurella multocida

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<400> 69
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Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
20 25 30

Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
35 40 45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
50 55 60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
65 70 75 80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
85 90 95

Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
100 105 110

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
115 120 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
130 135 140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145 150 155 160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
165 170 175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
180 185 190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
195 200 205

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Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
 210 215 220
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
 225 230 235 240
 His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
 385 390 395 400
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
 405 410 415

<210> 70
 <211> 3501
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (298)..(1905)

<220>
 <223> yabk

<400> 70
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gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180
cttagagcca cccaaatgaa cagcaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240
gtcaaaaat ggattgctgt ttggcaaacg accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt	345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	
1 5 10 15	
ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc	393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg	441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Trp Ala Leu	
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg gcc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt	633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
100 105 110	
tta tta gcc gtg tat gcc gct tct gcc tgg tta gcg atg tta agc cag	681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
115 120 125	
ttt ttc gct tgg gat tgg act cct aat att tac gcc tta aca ggt att	729
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
130 135 140	
tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt	777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
145 150 155 160	
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
195 200 205	
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt gcc gga ccg aaa	969
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Pro Lys	
210 215 220	
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
225 230 235 240	
gat gta ccg aaa gcc gcc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys	
245 250 255	

ttt ctg tta	ttc acg ctg	agt agc	ttt ttt tct	cca gcc	ccc gcc	acg	1113
Phe Leu Leu	Phe Thr Leu	Ser Ser	Phe Phe Ser	Pro Ala	Pro Ala	Thr	
	260		265		270		
aca tta cac	agt caa cct	act tgg	ttt gcg	ccc caa	tcg tat	tgg gtt	1161
Thr Leu His	Ser Gln Pro	Thr Trp	Phe Ala	Pro Gln	Ser Tyr	Trp Val	
	275		280		285		
aaa tta tgg	caa cgt	atg atc	att gtg	tgt gcg	aca gta	ttt atc	1209
Lys Leu Trp	Gln Arg Met	Ile Ile	Val Val	Cys Cys	Thr Val	Phe Ile	Leu
	290		295		300		
tta cgg cta	ctc aat	acg cta	ggt tct	gct ttg	ctt tcg	tct cag	1257
Leu Pro Leu	Leu Asn Thr	Leu Val	Val Ser	Ala Ala	Leu Ser	Ser Gln	Phe
	305		310		315		320
ttt acc ttg	tgg tta	caa cct	caa tta	tgg aaa	gca tta	ggt tac	1305
Phe Thr Leu	Trp Gln Pro	Gln Leu	Trp Lys	Ala Ala	Leu Gly	Tyr Ser	
	325		330		335		
ctc acc atc	gcc ccc	act tct	gca ttg	ctc gct	tta gta	ctg tct	1353
Leu Thr Ile	Ala Pro Thr	Ser Ala	Leu Leu	Ala Ala	Leu Val	Ser Phe	
	340		345		350		
gcc tta tta	ttg ctt	gcc aga	gaa tta	cat tgg	cga cat	tat cgc	1401
Ala Leu Leu	Leu Leu Ala	Arg Glu	Leu His	Trp Arg	His Tyr	Arg Ser	
	355		360		365		
tta tcc cat	gtg att	tta aat	atc ggt	gcg acc	att tta	gcc att	1449
Leu Ser His	Val Ile	Leu Asn	Ile Gly	Ala Thr	Ile Leu	Ala Ile	Pro
	370		375		380		
acg tta gtg	tta gct	att ggt	tta ttc	att tta	tta cgt	gag atc	1497
Thr Leu Val	Leu Ala	Ile Gly	Leu Phe	Ile Leu	Leu Arg	Glu Ile	Asp
	385		390		395		400
ttt tct cca	tac cat	ctt ttt	ggg gtt	gtg gta	tgc tgt	aac gcg	1545
Phe Ser Pro	Tyr His	Leu Phe	Gly Val	Val Val	Cys Cys	Asn Ala	Leu
	405		410		415		
gct gct atg	cct ttt	gtg ttg	cgt att	ttg gct	tta ccg	atg cat	1593
Ala Ala Met	Pro Phe	Val Leu	Arg Ile	Leu Ala	Leu Pro	Met His	Asn
	420		425		430		
aat atg att	tat tat	gaa aaa	tta tgc	caa tca	ctt aac	ctg cgt	1641
Asn Met Ile	Tyr Tyr	Glu Lys	Leu Cys	Gln Ser	Leu Asn	Leu Arg	Gly
	435		440		445		
tgg caa cgt	ttt cga	ttg att	gaa tgg	cac aag	ctt cgt	gcg cca	1689
Trp Gln Arg	Phe Arg	Leu Ile	Glu Trp	His Lys	Leu Arg	Ala Pro	Met
	450		455		460		
aaa tac gcc	ttt gca	ctg gct	tgt gcg	tta tca	tta ggc	gat ttc	1737
Lys Tyr Ala	Phe Ala	Leu Ala	Cys Ala	Leu Ser	Leu Gly	Asp Phe	Thr
	465		470		475		480
gca atc gcg	tta ttt	ggt cag	gct gac	ttc aca	tcg tta	ccg cat	1785
Ala Ile Ala	Leu Phe	Gly Gln	Ala Asp	Phe Thr	Ser Leu	Pro His	Leu
	485		490		495		
ttg tat caa	caa ttg	ggg cat	tat cgt	agt cag	gaa gcg	gca gta	1833
Leu Tyr Gln	Gln Leu	Gly His	Tyr Arg	Ser Gln	Glu Ala	Ala Val	Thr
	500		505		510		

gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa 1881
 Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
 515 520 525

cga cat cag gaa cgg cgt gat gat taatttaaacc ggtgttcagt tttcctataa 1935
 Arg His Gln Glu Pro Arg Asp Asp
 530 535

tacctttact tttgagctgg atttgcagat tctgtctcaa caaaaagttg ctattattgg 1995
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 gcaaggggaa atttggttga atgggtgaaa tcatagccaa actcaacctt atgaacgtcc 2115
 ggtatctatt ttgtttcaag aaaacaactt gtttacgcat ttgactgtgg cagagaatat 2175
 ggcattaggg ctgaaaccaa gcctaaaact gaccgcactt gaacaacaac gcgtacaaca 2235
 agtggaagt gcagtggtt tgacgggttt tcttaataca taccaccacc agttatcggg 2295
 tgggcaaaaa cagcgtgtgg cgttggcggc ttgtttatta cgcgataaag caattttgtt 2355
 atgggatgaa cctttttctg ccttagatcc cgatttacgg gcagaaatgt tgcattttatt 2415
 gttacagttg tgtgatgaaa aaaaattaac actcctgac gtgacacatc aagtgaacga 2475
 attacagcag aaaatggatc gtatgattcg ttttgaacat ggtaggatga gtgagtcacc 2535
 ctttttgaag gataatttta acgaaaaaca gaccgcactt taggcggctt attaattaga 2595
 taaggaaa gaataatatt tctgtgtgta aaattgaagc cctgttttag accccttttt 2715
 tagatttggg ttatcgggct gcgcaagtgc accgagaaaa cttaatacct aaagccattc 2775
 aattatccac ttaatgtcg attaaaaagg ggggatgtcc agaggattgt ggctactgtc 2835
 cgcagtcagc acgttatcat actggagtag aaaagcagca attactcgat gtggaagaaa 2895
 ttgttgaaaa agccaaaatt gccaaagcac gtggtgcagg gcgcttttgt atggggggctg 2955
 catggcgtgg accgaaacgg aaagacattg aaaaagtac gcgaatcatt aaagcgggtga 3015
 aagaactggg cttagaaacc tgtgttacct ttggtttatt gcaagatggg atggcagaag 3075
 atttaaaaga agcggggttg gattattata accataatct cgatcacagc ccagaaacct 3135
 acggtaattg gattgtgacc cgtcaatttg atgatcgat taatacgtta ggtaaagtgc 3195
 gtaaaagctg cttaaaagtg tctgtggcgg ggattattgg catgaatgaa acccgtaaag 3255
 aaagagcagg attaatgtct agcttagcta atttagacc gccaccgaa tcggtgccga 3315
 ttaatcaatt agtgaaagt gaaggtacc ctttagccga tgcggcagaa ttagactgga 3375
 cagaatttgt gcgcactatt gcggtggcgc gtattaccat gccgaaaagc tatgtacgtt 3435
 tatcagcagg gcgtcaaggc atgtcggaag aaatgcaagc catgtgcttt atggctggcg 3495
 cgaatt 3501

<210> 71
 <211> 536
 <212> PRT
 <213> *Pasteurella multocida*

<400> 71

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Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
 1             5             10             15

Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
      20             25             30

Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
      35             40             45

Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
      50             55             60

Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
      65             70             75             80

Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
      85             90             95

Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
      100            105            110

Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
      115            120            125

Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
      130            135            140

Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
      145            150            155            160

Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
      165            170            175

Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
      180            185            190

Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
      195            200            205

Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys
      210            215            220

Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
      225            230            235            240

Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
      245            250            255

Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
      260            265            270

Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
      275            280            285

Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
      290            295            300
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
305                      310                      315                      320

Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
                      325                      330                      335

Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Val Leu Ser Phe
                      340                      345                      350

Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
                      355                      360                      365

Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro
                      370                      375                      380

Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
385                      390                      395                      400

Phe Ser Pro Tyr His Leu Phe Gly Val Val Cys Cys Asn Ala Leu
                      405                      410                      415

Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
                      420                      425                      430

Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
                      435                      440                      445

Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
                      450                      455                      460

Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
465                      470                      475                      480

Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
                      485                      490                      495

Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
                      500                      505                      510

Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
                      515                      520                      525

Arg His Gln Glu Pro Arg Asp Asp
530                      535

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<210> 72
<211> 3182
<212> DNA
<213> Pasteurella multocida

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<220>
<221> CDS
<222> (1544)..(2809)

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<220>
<223> ygiK

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<220>
<221> misc_feature
<222> 452
<223> N = A or T or G or C

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cttcatgtca ctttcagttt cagctgcaga aattaatttg aaatttgaaa gtctgaattt 120
tgcaggagaa aaagtttatg aaatccaaaa agaattggact gacaatatgg aaaaagcttc 180
caatgggaga ataagtatag agttattacc tctcgactca gtcttaaaat ctagtacat 240
gctttctggg gtctgaaata aaattattga tggagcgggt gcaacagcgg caatgtatgc 300
aggcactgac cctggattcg gattaattgg tgatactatt tctgcttgga accatgacga 360
agatatttta aatttttact ataattggagg tgggtttgaa gttgttgata atattttcca 420
acaatatggg gccaaactca ttggtgtatc anttacggga gcagaatcat taccatcgaa 480
agtaaaaaa gctaatactg aagattttta aggtataaaa attcgggctc cctctggctc 540
tatecaaaaa ttgtttgcaa gattaggagc cgctcctggt ggtcttctcg gtccagaaat 600
ctatactagt ttgaaaaag gtattattga tgcctccgat ttctcaacgt ttgcaataaa 660
tcaagcacia ggagtcacat atattgcaa ataccaatc tatccgggaa ttcattcttc 720
accagccggt catatgatta tgaatcataa aacttggagt agcttaactc catcggatca 780
agcattctta attgcttact ttaaagggat ggctctcgat actctgactc gtgctcatta 840
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gagaagcatt atttactcca tcaggaaaaa tcaaatgca aacttctgga agtgtattag 1500
acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
                               Met Pro His His
                               1

tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata 1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
5          10          15          20

tca gga gga att atc atg ata agt gca ttt ggg ata ggt att gga act 1651
Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
          25          30          35

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ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca 1699
 Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro
 40 45 50

tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg 1747
 Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile Ser Tyr Leu Trp
 55 60 65

ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat 1795
 Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp
 70 75 80

ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg 1843
 Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met
 85 90 95 100

gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca 1891
 Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala
 105 110 115

atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tgc 1939
 Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser
 120 125 130

atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga 1987
 Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly
 135 140 145

gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta 2035
 Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu
 150 155 160

ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca 2083
 Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala
 165 170 175 180

ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg 2131
 Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met
 185 190 195

acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc 2179
 Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala
 200 205 210

tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc 2227
 Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys
 215 220 225

tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat 2275
 Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Ser Ser Glu Asn His
 230 235 240

aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att 2323
 Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile His Asp Ile Ala Ile
 245 250 255 260

cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata 2371
 Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile
 265 270 275

gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta 2419
 Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu
 280 285 290

gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca 2467
 Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser
 295 300 305
 cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att 2515
 Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile
 310 315 320
 ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga 2563
 Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg
 325 330 335 340
 ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act 2611
 Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr
 345 350 355
 atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat 2659
 Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp
 360 365 370
 tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca 2707
 Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr
 375 380 385
 atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc 2755
 Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro
 390 395 400
 tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt 2803
 Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly
 405 410 415 420
 act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt 2859
 Thr Phe
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<210> 73

<211> 422

<212> PRT

<213> Pasteurella multocida

<400> 73

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 Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe
 35 40 45

Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile
 50 55 60
 Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
 65 70 75 80
 Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
 85 90 95
 Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
 100 105 110
 Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
 115 120 125
 Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly
 130 135 140
 Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln
 145 150 155 160
 Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val
 165 170 175
 Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile
 180 185 190
 Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala
 195 200 205
 Ala Ile Pro Ala Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile
 210 215 220
 Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser
 225 230 235 240
 Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His
 245 250 255
 Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile
 260 265 270
 Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val
 275 280 285
 Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile
 290 295 300
 Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile
 305 310 315 320
 Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met
 325 330 335
 Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser
 340 345 350
 Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly
 355 360 365
 Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr
 370 375 380

Ser Lys Ala Thr ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
385 390 395 400

Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
405 410 415

Val Gly Arg Gly Thr Phe
420

<210> 74
<211> 2787
<212> DNA
<213> *Pasteurella multocida*

<220>
<221> CDS
<222> (463)..(936)

<220>
<223> yhcJ

<400> 74
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ggcggtgc aa tctgttgccg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
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gatcctacgg tgacagagta agcacaatc tcaattgcgg ttttcgccaa ttctgggggtg 360
ttatagcgcc ctcttgccat cactcggcag ccagcagcat tcaaatcttt gactaaactga 420
taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca 474
Met Val Leu Pro
1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
5 10 15 20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
25 30 35

atg gct tca cgt gta gtt gga cgg acg cga tgg gta cca tca aaa gca 618
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
40 45 50

ata ata tgg cgg cct gct cgg gct aac tct tca atg tct tgt aaa aat 666
Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tgg cgt tta acg ata cca 714
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tgg atc 762
Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile

85	90	95	100			
cct tca ata cgt aac	ccg gca gca	cca ccg ata acg gat gct tgc gcc	810			
Pro Ser Ile Arg Asn	Pro Ala Ala	Pro Ile Thr Asp Ala Cys Ala				
	105	110	115			
atg gcg gca aca att	tct ggc gag	tcc att ggc cca tta tct acg ggc	858			
Met Ala Ala Thr Ile	Ser Gly Glu	Ser Ile Gly Pro Leu Ser Thr Gly				
	120	125	130			
tgg caa gat gcg att aag cca tat	tta att tgt tct aaa act tgc gga	906				
Trp Gln Asp Ala Ile Lys	Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly					
	135	140	145			
tgt gat agt ttt gac ata tta act	cca gtc taaatttacc	aaaagaagat	956			
Cys Asp Ser Phe Asp Ile Leu Thr	Pro Val					
	150	155				
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cacgtttcca	aatttacttc	ccagaagcag	aagtatttgc	gttgccctat	atgattccta	2276
attttgaac	ctctaaaaaa	gcgttgctcg	acacaaaatt	tggtcaaggt	ttattgaaaa	2336

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 acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696
 atttacaaaa agtgggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756
 tcgttgacgg tgagaacacg ttagtgtaat t 2787

<210> 75
 <211> 158
 <212> PRT
 <213> Pasteurella multocida

<400> 75
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 20 25 30
 Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val
 35 40 45
 Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met
 50 55 60
 Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
 65 70 75 80
 Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Leu Arg Val Ala Phe
 85 90 95
 Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
 100 105 110
 Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
 115 120 125
 Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser
 130 135 140
 Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
 145 150 155

<210> 76
 <211> 2787
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1949)..(2785)

<220>

<223> yiaO

<400> 76

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ggcgttgcaA tctgttgGcg ttgtttctatt ttgcgctctg ttacaatagc cgaggcaatt 180
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taatccggtt cagctggaat ttcaccgcca gtataaccag acatgggtct accaataatt 480
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gcagcaccac cgataacgga tgcttgcgcc atggcggcaa caatttctcg cgagtccatt 840
ggccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900
tgcggaatgt atagttttga catattaaCt ccagtctaaa tttatcaaaa gaagattgac 960
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Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu	95	100	105	110
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<212> PRT

<213> Pasteurella multocida

<400> 81

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Glu Leu Thr Glu Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr
 35 40 45

Cys Ser Ile Arg Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly
 50 55 60

Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val
 65 70 75 80

Gly Gly Cys Val Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala
 85 90 95

Pro Tyr Val Asp Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro
 100 105 110

Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val
 115 120 125

Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala
 130 135 140

Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr
 145 150 155 160
 Cys Ser Phe Cys Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg
 165 170 175
 Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly
 180 185 190
 Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly
 195 200 205
 Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu
 210 215 220
 Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His
 225 230 235 240
 Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro
 245 250 255
 Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
 260 265 270
 Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser
 275 280 285
 Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser
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 Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln
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 Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg
 355 360 365
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 370 375 380
 Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
 385 390 395 400
 Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
 405 410 415
 Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
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 Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
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<213> Pasteurella multocida

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Met Lys Lys
1

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Thr Val Val Asn Pro Glu Arg Arg Phe Phe Lys Glu Ala Thr Arg
5 10 15

act gca ggc ggg ttg gca ggg gtg act ttg ctc ctt ggt ttg caa caa 511
Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly Leu Gln Gln
20 25 30 35

aag cag agt ctt gcg cgc gaa ggc gtg gcg tta cgc cca cct ttt gcc 559
Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
40 45 50

ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgt ggt cag 607
Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
55 60 65

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Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
70 75 80

tca cag atg gaa gca ggt aca cag tat ttc att gcg cgc gat aag ccc 703
Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
85 90 95

tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt 751
Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
100 105 110 115

gca ttg gat aat caa gca aca gaa atc gat gat gcg cgt atg ggg tta 799
Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg Met Gly Leu
120 125 130

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Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg

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tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc 943			
Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile			
165	170	175	
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Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu			
180	185	190	195
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Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu			
200	205	210	
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Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys			
215	220	225	
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Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro			
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245	250		
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<211> 250

<212> PRT

<213> Pasteurella multocida

<400> 83

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 35 40 45
 Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg
 50 55 60
 Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala
 65 70 75 80
 Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
 85 90 95
 Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys
 100 105 110
 Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg
 115 120 125
 Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
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 Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys
 145 150 155 160
 Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala
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Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
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Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
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Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
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Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
      15          20          25
atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt etc 2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
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tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
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 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
 95 100
 gtcaagact actgagtaac gcttgtagtc gcgtgaatcg actgtttacat aagccgatat 2799
 gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttgg 2859
 cgataaagcg tcaaacgaaa gcacgacttt accgtccttg acttccacct gatcttcaat 2919
 gagcacttga cttagtgcga ccaatcgacc gttggcagtc agtgcgcgaa tgccgtgatc 2979
 cgtatcaagc gttacaccgc tattttttcc ccagttttta ttgagctttt cactatgttt 3039
 cagtaagttt ctgccaccaa tctgcaactg attaaactta gttcaagcg tttcactctt 3099
 gactgcaagc gacttggttt cattgctaac cgtctgctca agtgcgtgta ttttgatgt 3159
 taaactcaac ttagtgtcat tgacttcac agtccattct gactttaact cttttctcgc 3219
 aagtgaagcc acttcacttt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279
 attttgcgcc actttagaat cgagcgtttc tagttttgta gagaaagatt tgcctttttc 3339
 gctagccggt ttttgaaata gctgtatttc actttcgctc aatccaactc tagcagttag 3399
 actgcttagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459
 aatatccgcg cttacttcgc agatagccac gtcga 3494

<210> 85

<211> 103

<212> PRT

<213> Pasteurella multocida

<400> 85

Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr
 1 5 10 15

Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile
 20 25 30

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly
 35 40 45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
 50 55 60

Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser
 65 70 75 80

Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr
 85 90 95

Ile Ser Thr Leu Asn Arg Val

100

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 86
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19

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 87
cggccggtac cggcctagg

19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
catggtacc attctaac

18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctaggtaacct acaacctc

18

<210> 90
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
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<222>
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insert

<220>

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 <222> 93
 <223> N = A or T or G or C

<400> 90
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 nknknknknk nknknknknk nknknknknk nknkaagctt ggtagaatg ggtaccatg 119

<210> 91
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 91
tacctacaac ctcaagct 18

<210> 92
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
taccctattct aaccaagc 18

<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
tacctacaac ctcaagctt 19

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
taccctattct aaccaagctt 20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac 19

<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc 27

<210> 97
 <211> 531
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

<220>
 <223> atpG

<400> 97
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 cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120
 agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcgggtt acgtcgctta 180
 caaccgtttt gaaaatacga tgtcacaaaa acctgttacc gcacagttac ttccgttacc 240
 taaactagat gacgatgaat tagatacgaa aggttcattg gattatattt atgaaccgaa 300
 tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
 agttgtagat aacctagctt ctgaacaagc cgctcgaaat gtagcgtatg aagccgcaac 420
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcaccaagc 480
 aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 98
 tctccattcc cttgtcgcgg caccc 25

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 99
 ggattacagc cggatccggg 20

<210> 100
 <211> 1034
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> cap5E

<220>
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 <222> (1)..(1032)

<400> 100
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 1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
 Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
 20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144
 Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
 35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
 Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
 50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
 Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
 65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat cgg tta gag gca 288
 Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
 85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
 Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
 100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
 Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
 115 120 125

tac cca att aat gcg atg gcc att tct aaa gca atg atg gaa aaa gtc 432
 Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
 130 135 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480
 Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
 145 150 155 160

tgt act cgc tat gcc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528
 Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
 165 170 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
 180 185 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
 195 200 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
 210 215 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
 225 230 235 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

245	250	255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat			816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His			
260	265	270	
gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt			864
Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser			
275	280	285	
tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa			912
Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Pro Lys Ile Thr Glu			
290	295	300	
gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa			960
Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu			
305	310	315	320
atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag			1008
Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu			
325	330	335	
ggt gaa tac atc tca ccg gag gta ta			1034
Gly Glu Tyr Ile Ser Pro Glu Val			
340			
 <210> 101			
<211> 344			
<212> PRT			
<213> Pasteurella multocida			
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Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile			
20	25	30	
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys			
35	40	45	
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr			
50	55	60	
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala			
65	70	75	80
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala			
85	90	95	
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ile			
100	105	110	
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val			
115	120	125	
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val			
130	135	140	
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys			
145	150	155	160

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
 165 170 175
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
 180 185 190
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
 195 200 205
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
 210 215 220
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
 225 230 235 240
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His
 245 250 255
 Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His
 260 265 270
 Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser
 275 280 285
 Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu
 290 295 300
 Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu
 305 310 315 320
 Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu
 325 330 335
 Gly Glu Tyr Ile Ser Pro Glu Val
 340

<210> 102
 <211> 4931
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> fhaB2

<220>
 <221> CDS
 <222> (1)..(4929)

<220>
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 <222> 1632
 <223> Xaa = any or unknown amino acid

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 1 5 10 15
 ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser

20	25	30	
tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu 35 40 45			144
cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Val Lys Ser Thr 50 55 60			192
ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser 65 70 75 80			240
att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys 85 90 95			288
ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile 100 105 110			336
aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr 115 120 125			384
caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly 130 135 140			432
aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser 145 150 155 160			480
gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu 165 170 175			528
att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala 180 185 190			576
gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val 195 200 205			624
ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn 210 215 220			672
caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg 225 230 235 240			720
ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu 245 250 255			768
aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr 260 265 270			816
gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag			864

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	
355 360 365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	
370 375 380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	
385 390 395 400	
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	
405 410 415	
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475 480	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	

ttt tta ggc tct cgc ttt ttc tca ata tct cgc tcg atg ctc gca agc Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser 530 535 540	1632
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu 545 550 555 560	1680
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu 565 570 575	1728
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn 580 585 590	1776
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala 595 600 605	1824
aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr 610 615 620	1872
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile 625 630 635 640	1920
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr 645 650 655	1968
gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn 660 665 670	2016
ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser 675 680 685	2064
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat Val Tyr Asn Ile Gly Asp Ile Tyr Thr Ala Ser Lys Lys Leu Thr Val His 690 695 700	2112
act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr 705 710 715 720	2160
aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val 725 730 735	2208
cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu 740 745 750	2256
caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct Gln Asp Lys Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser 755 760 765	2304
gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser 770 775 780	2352

aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe 785 790 795 800	2400
aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln 805 810 815	2448
aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr 820 825 830	2496
tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala 835 840 845	2544
tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly 850 855 860	2592
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser 865 870 875 880	2640
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys 885 890 895	2688
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp 900 905 910	2736
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe 915 920 925	2784
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu 930 935 940	2832
ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys 945 950 955 960	2880
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser 965 970 975	2928
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp 980 985 990	2976
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu 995 1000 1005	3024
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gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser 1025 1030 1035 1040	3120

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His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser	
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Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met	
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ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca	3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro	
1075 1080 1085	
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt	3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe	
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Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu	
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gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa	3456
Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys	
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gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag	3504
Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Glu Glu	
1155 1160 1165	
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga	3552
Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg	
1170 1175 1180	
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Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Glu Gln Glu Lys Arg Val	
1185 1190 1195 1200	
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Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala	
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Lys Gln Val Glu Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg	
1220 1225 1230	
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Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys	
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1285 1290 1295	

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Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	
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Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys	
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Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln	
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Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln	
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Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn	
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Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe	
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Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	
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Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	
1475 1480 1485	
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1490 1495 1500	
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tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg	4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	
1540 1545 1550	

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gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc 4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
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Ser Ala Leu Gln Val Ala  Glu Leu Asp Val Ala  Gly Leu Lys Val Pro
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ctt tta ggc gtg tcc  gtc tcc atc cag ttt  att cag agc ata cta gtg 4848
Leu Leu Gly Val Ser  Val Ser Ile Gln Phe  Ile Gln Ser Ile Leu Val
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Arg Gln Leu Gln Gln  Glu Gly Ser Ile Phe  Glu Val Gly His Leu His Xaa
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Ala Val Asp  Arg Arg Cys Glu Pro  Ser Gly Glu
      1635                      1640

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<213> Pasteurella multocida

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<221> misc_feature

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Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
      35          40          45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
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Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
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Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
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Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
      100          105          110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
      115          120          125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
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Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
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 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
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 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
 225 230 235 240
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
 245 250 255
 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
 260 265 270
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
 275 280 285
 Gln Ser Ile, Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
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 305 310 315 320
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
 325 330 335
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
 340 345 350
 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
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 370 375 380
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
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 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
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 545 550 555 560
 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
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 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
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 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
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 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
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 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
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 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
 660 665 670
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
 675 680 685
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 690 695 700
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
 705 710 715 720
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
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 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
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 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
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 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
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 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
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 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
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 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
 930 935 940
 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
 945 950 955 960
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115 120 125	
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130 135 140	
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165 170 175	
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260 265 270	
ggg ccg agt cgc cat cgt tta tct gcg aaa ttc gaa ttt cgt gat aag Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys	864
275 280 285	
ttt tta gaa aat atg aat aag cat ttt acg ttt cgg ccg tgg caa atc Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile	912
290 295 300	
aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro	960
305 310 315	
gtt aaa tcc cga gag ttt tct ttt tct ctt atg gac gac att aag att Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile	1008
325 330 335	

ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg tgg gat cac tat aac	1056
Gly Glu Leu Leu His Leu Gly Leu Gly Arg Trp Asp His Tyr Asn	
340 345 350	
tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga	1104
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg	
355 360 365	
tta cct tat cca aaa aca tca tcc aaa ttt tgg tat caa ttg agt tta	1152
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu	
370 375 380	
gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc	1200
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr	
385 390 395 400	
ggg ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga	1248
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly	
405 410 415	
aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act	1296
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
420 425 430	
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat	1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His	
435 440 445	
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa	1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu	
450 455 460	
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat	1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr	
465 470 475 480	
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa	1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu	
485 490 495	
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tgg gca	1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala	
500 505 510	
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc	1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser	
515 520 525	
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg	1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
530 535 540	
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt	1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser	
545 550 555 560	
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa	1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta	1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu	
580 585 590	

agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt 1824
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605
 aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat 1872
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620
 tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640
 tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655
 cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
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<210> 105

<211> 669

<212> PRT

<213> Pasteurella multocida

<400> 105

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Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
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Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
 165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240
 Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
 290 295 300
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
 305 310 315 320
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
 325 330 335
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
 340 345 350
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
 355 360 365
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
 370 375 380
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
 385 390 395 400
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
 405 410 415
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
 420 425 430
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
 435 440 445
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
 450 455 460
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
 465 470 475 480
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
 485 490 495
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
 500 505 510
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
 515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
 530 535 540
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
 545 550 555 560
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
 565 570 575
 Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
 580 585 590
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
 660 665

<210> 106

<211> 908

<212> DNA

<213> Pasteurella multocida

<220>

<223> lgtC

<220>

<221> CDS

<222> (1)..(906)

<400> 106

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 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
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gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta	288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu	
85 90 95	
aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta	336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu	
100 105 110	
gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt	384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys	
115 120 125	
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att	432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile	
130 135 140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt	480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe	
145 150 155 160	
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac	528
Asn Leu Asp Glu Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
165 170 175	
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata	576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile	
180 185 190	
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt	624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe	
195 200 205	
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga	672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly	
210 215 220	
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt	720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val	
225 230 235 240	
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa	768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys	
245 250 255	
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga	816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg	
260 265 270	
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc	864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala	
275 280 285	
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta	908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr	
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<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

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Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
          20           25           30
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
      35           40           45
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
      50           55           60
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
      65           70           75           80
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
          85           90           95
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
      100           105           110
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
      115           120           125
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
      130           135           140
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
      145           150           155           160
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
      165           170           175
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
      180           185           190
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
      195           200           205
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
      210           215           220
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
      225           230           235           240
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
      245           250           255
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
      260           265           270
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
      275           280           285
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
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<210> 108

<211> 2054

<212> DNA

<213> Pasteurella multocida

<220>

<223> pnp

<220>

<221> CDS

<222> (1) .. (2052)

<400> 108

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1				5				10						15		

aaa	gat	gtg	aaa	gaa	ggg	caa	gac	ttc	ttc	cca	tta	act	gtt	aac	tat	96
Lys	Asp	Val	Lys	Glu	Gly	Gln	Asp	Phe	Phe	Pro	Leu	Thr	Val	Asn	Tyr	
		20						25					30			

caa	gag	cgt	act	tat	gct	gca	ggc	cgt	att	cct	ggg	ggc	ttt	ttc	aaa	144
Gln	Glu	Arg	Thr	Tyr	Ala	Ala	Gly	Arg	Ile	Pro	Gly	Gly	Phe	Phe	Lys	
		35					40					45				

cgt	gaa	ggg	cgt	cct	tct	gaa	ggc	gaa	act	tta	att	gct	cgt	tta	att	192
Arg	Glu	Gly	Arg	Pro	Ser	Glu	Gly	Glu	Thr	Leu	Ile	Ala	Arg	Leu	Ile	
	50					55					60					

gac	cgt	cca	att	cgt	cct	ctt	ttc	cca	gaa	ggg	ttt	tat	aac	gaa	atc	240
Asp	Arg	Pro	Ile	Arg	Pro	Leu	Phe	Pro	Glu	Gly	Phe	Tyr	Asn	Glu	Ile	
	65				70					75				80		

caa	atc	gtg	gcg	aca	gtg	gtg	tct	gtt	aat	ccg	caa	att	tgt	cca	gat	288
Gln	Ile	Val	Ala	Met	Ile	Val	Val	Ser	Val	Asn	Pro	Gln	Ile	Cys	Pro	
			85						90					95		

tta	gtg	gca	atg	atc	ggg	gca	tct	gcg	gca	ctt	tct	tta	tca	ggg	gtg	336
Leu	Val	Ala	Met	Ile	Gly	Ala	Ser	Ala	Ala	Leu	Ser	Leu	Ser	Gly	Val	
		100						105					110			

cca	ttt	aat	ggc	cct	atc	ggg	gcg	gca	cgt	gtt	ggg	ttt	att	gat	gat	384
Pro	Phe	Asn	Gly	Pro	Ile	Gly	Ala	Ala	Arg	Val	Gly	Phe	Ile	Asp	Asp	
		115					120					125				

caa	ttt	gtg	tta	aac	cca	acc	atg	aac	gag	caa	aaa	caa	agc	cgt	tta	432
Gln	Phe	Val	Leu	Asn	Pro	Thr	Met	Asn	Glu	Gln	Lys	Gln	Ser	Arg	Leu	
		130				135					140					

gac	ttg	gtt	gtc	gcg	gga	aca	gat	aaa	gcg	gtg	tta	atg	gtg	gaa	tct	480
Asp	Leu	Val	Val	Ala	Gly	Thr	Asp	Lys	Ala	Val	Leu	Met	Val	Glu	Ser	
	145				150				155					160		

gaa	gcc	gat	gta	tta	acc	gaa	gaa	caa	atg	tta	gct	gcg	gtg	gtg	ttt	528
Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe	
			165						170					175		

ggg	cat	cag	caa	caa	caa	gtg	gtg	att	gac	gcg	atc	aaa	gaa	ttt	acc	576
Gly	His	Gln	Gln	Gln	Gln	Val	Val	Ile	Asp	Ala	Ile	Lys	Glu	Phe	Thr	
		180						185					190			

gca	gaa	gcc	ggg	aaa	ccg	cgt	tgg	gat	tgg	gtg	gca	cct	gaa	cca	aat	624
Ala	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	Val	Ala	Pro	Glu	Pro	Asn	
		195				200						205				

acc	gcg	tta	att	gaa	aaa	gtg	aaa	gcg	att	gca	gaa	gcg	cgt	tta	ggc	672
Thr	Ala	Leu	Ile	Glu	Lys	Val	Lys	Ala	Ile	Ala	Glu	Ala	Arg	Leu	Gly	
		210				215						220				

gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp	720
225 230 235 240	
gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu	768
245 250 255	
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu	816
260 265 270	
gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile	864
275 280 285	
gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly	912
290 295 300	
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr	960
305 310 315 320	
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile	1008
325 330 335	
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr	1056
340 345 350	
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro	1104
355 360 365	
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala	1152
370 375 380	
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val	1200
385 390 395 400	
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tgc gtt tgt Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys	1248
405 410 415	
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala	1296
420 425 430	
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val	1344
435 440 445	
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp	1392
450 455 460	
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp	1440
465 470 475 480	

atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac 1488
 Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495

caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg 1536
 Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala 500 505 510

atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac 1584
 Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr 515 520 525

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt 1632
 Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly 530 535 540

ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat 1680
 Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp 545 550 555 560

atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca 1728
 Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser 565 570 575

gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa 1776
 Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu 580 585 590

gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt 1824
 Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly 595 600 605

gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct 1872
 Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser 610 615 620

caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg 1920
 Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val 625 630 635 640

ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt 1968
 Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg 645 650 655

att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat 2016
 Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp 660 665 670

tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta 2054
 Ser Val Val Ala Asp Val Ala Glu Glu Asn Ala 675 680

<210> 109

<211> 684

<212> PRT

<213> Pasteurella multocida

<400> 109

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
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		35					40					45			
Arg	Glu	Gly	Arg	Pro	Ser	Glu	Gly	Glu	Thr	Leu	Ile	Ala	Arg	Leu	Ile
	50					55					60				
Asp	Arg	Pro	Ile	Arg	Pro	Leu	Phe	Pro	Glu	Gly	Phe	Tyr	Asn	Glu	Ile
65					70					75				80	
Gln	Ile	Val	Ala	Thr	Val	Val	Ser	Val	Asn	Pro	Gln	Ile	Cys	Pro	Asp
			85						90					95	
Leu	Val	Ala	Met	Ile	Gly	Ala	Ser	Ala	Ala	Leu	Ser	Leu	Ser	Gly	Val
		100						105					110		
Pro	Phe	Asn	Gly	Pro	Ile	Gly	Ala	Ala	Arg	Val	Gly	Phe	Ile	Asp	Asp
		115					120					125			
Gln	Phe	Val	Leu	Asn	Pro	Thr	Met	Asn	Glu	Gln	Lys	Gln	Ser	Arg	Leu
	130					135					140				
Asp	Leu	Val	Val	Ala	Gly	Thr	Asp	Lys	Ala	Val	Leu	Met	Val	Glu	Ser
145					150					155				160	
Glu	Ala	Asp	Val	Leu	Thr	Glu	Glu	Gln	Met	Leu	Ala	Ala	Val	Val	Phe
			165					170						175	
Gly	His	Gln	Gln	Gln	Gln	Val	Val	Ile	Asp	Ala	Ile	Lys	Glu	Phe	Thr
		180						185					190		
Ala	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp	Val	Ala	Pro	Glu	Pro	Asn
		195				200					205				
Thr	Ala	Leu	Ile	Glu	Lys	Val	Lys	Ala	Ile	Ala	Glu	Ala	Arg	Leu	Gly
	210					215					220				
Glu	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala	Arg	Tyr	Glu	Gln	Ile	Asp
225					230					235				240	
Ala	Ile	Lys	Ala	Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu
			245					250						255	
Gly	Glu	Asp	Ile	Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu
	260							265					270		
Glu	Ser	Gln	Ile	Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile
	275					280						285			
Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly
	290					295					300				
Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr
	305					310					315				320
Gln	Ala	Leu	Ala	Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile
			325					330						335	
Ile	Asp	Glu	Leu	Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr
	340						345					350			
Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro

355	360	365
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380		
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400		
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys 405 410 415		
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430		
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445		
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460		
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480		
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495		
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala 500 505 510		
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr 515 520 525		
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly 530 535 540		
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp 545 550 555 560		
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser 565 570 575		
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu 580 585 590		
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly 595 600 605		
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser 610 615 620		
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val 625 630 635 640		
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg 645 650 655		
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp 660 665 670		
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala 675 680		

<210> 110
 <211> 1514
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> purF

<220>
 <221> CDS
 <222> (1)..(1512)

<400> 110
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 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15
 att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96
 Ile Tyr Asp Ala Leu Thr Leu Leu His Arg Gly Gln Asp Ala Ala
 20 25 30
 ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45
 aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
 50 55 60
 caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80
 tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
 85 90 95
 tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
 100 105 110
 gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125
 tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
 130 135 140
 aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
 145 150 155 160
 cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175
 cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
 180 185 190
 tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

195	200	205	
gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val	672		
210	215	220	
caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala	720		
225	230	235	240
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr	768		
245	250	255	
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr	816		
260	265	270	
gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg	864		
275	280	285	
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu	912		
290	295	300	
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa cgc Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro	960		
305	310	315	320
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile	1008		
325	330	335	
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn	1056		
340	345	350	
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp	1104		
355	360	365	
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg	1152		
370	375	380	
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile	1200		
385	390	395	400
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu	1248		
405	410	415	
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val	1296		
420	425	430	
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln	1344		
435	440	445	
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg	1392		

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460
 gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca 1440
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480
 gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc 1488
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495
 aat ctt gaa atg cac aat gaa aaa ta 1514
 Asn Leu Glu Met His Asn Glu Lys
 500

 <210> 111
 <211> 504
 <212> PRT
 <213> *Pasteurella multocida*

 <400> 111
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
 50 55 60
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
 85 90 95
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
 100 105 110
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
 130 135 140
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
 145 150 155 160
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
 180 185 190
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
 195 200 205
 Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val
 210 215 220

Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
 225 230 235 240
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
 245 250 255
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
 260 265 270
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
 275 280 285
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
 290 295 300
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
 305 310 315 320
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
 325 330 335
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
 340 345 350
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
 355 360 365
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
 370 375 380
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
 385 390 395 400
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
 405 410 415
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
 420 425 430
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
 435 440 445
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495
 Asn Leu Glu Met His Asn Glu Lys
 500

<210> 112
 <211> 989
 <212> DNA
 <213> *Pasteurella multocida*
 <220>
 <223> rci

<220>

<221> CDS

<222> (1)..(987)

<400> 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc	48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser	
1 5 10 15	
aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct	96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala	
20 25 30	
aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa	144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa	192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	

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aaa aac ggg cac tct aga gat gtg ccg ctt tgc caa aga gct gtt gcg 720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
225 230 235 240

cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag 768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
245 250 255

acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag 816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
260 265 270

tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg 864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
275 280 285

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
290 295 300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305 310 315 320

atg agt gaa gtg gca aac ttg ttg gat ta 989
Met Ser Glu Val Ala Asn Leu Leu Asp
325

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<210> 113

<211> 329

<212> PRT

<213> *Pasteurella multocida*

<400> 113

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Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
1 5 10 15

Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
20 25 30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
35 40 45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
50 55 60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
65 70 75 80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
85 90 95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
100 105 110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
115 120 125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
130 135 140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr

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145 150 155 160
 Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu
 165 170 175
 Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu
 180 185 190
 Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys
 195 200 205
 Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr
 210 215 220
 Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
 225 230 235 240
 Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
 245 250 255
 Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
 260 265 270
 Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
 275 280 285
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
 290 295 300
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
 305 310 315 320
 Met Ser Glu Val Ala Asn Leu Leu Asp
 325

<210> 114

<211> 1190

<212> DNA

<213> *Pasteurella multocida*

<220>

<223> sopE

<220>

<221> CDS

<222> (1)..(1188)

<400> 114

atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa 48
 Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
 1 5 10 15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
 20 25 30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc 144
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
 35 40 45

gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192
 Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Lys Gln

50	55	60	
ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc 240 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys 80 65 70 75			
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa 288 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu 95 85 90			
aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa 336 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu 110 100 105			
gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa 384 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys 125 115 120			
ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa 432 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys 140 130 135			
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt 480 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe 160 145 150 155			
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa 528 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln 175 165 170			
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat 576 Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp 190 180 185			
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc 624 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala 205 195 200			
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc 672 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly 220 210 215			
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc 720 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val 240 225 230			
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac 768 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn 255 245 250			
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt 816 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Val Asn His Asn Gly Phe 270 260 265			
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt 864 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe 285 275 280			
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg 912 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly 300 290 295			
gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa 960			

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys 1008
 305 310 315 320
 gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
 325 330 335
 ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
 340 345 350
 gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
 355 360 365
 cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
 370 375 380
 gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 115

<211> 396

<212> PRT

<213> Pasteurella multocida

<400> 115

Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
 1 5 10 15
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
 20 25 30
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
 35 40 45
 Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Lys Gln
 50 55 60
 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
 65 70 75 80
 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
 85 90 95
 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
 100 105 110
 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
 115 120 125
 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
 130 135 140
 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
 145 150 155 160
 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
 165 170 175

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Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
      180                      185                      190
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
      195                      200                      205
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
      210                      215                      220
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
      225                      230                      235                      240
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
      245                      250                      255
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
      260                      265                      270
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
      275                      280                      285
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
      290                      295                      300
Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
      305                      310                      315                      320
Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
      325                      330                      335
Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
      340                      345                      350
Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
      355                      360                      365
Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
      370                      375                      380
Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
      385                      390                      395

<210> 116
<211> 2204
<212> DNA
<213> Pasteurella multocida

<220>
<223> unkK

<220>
<221> CDS
<222> (1)..(2202)

<400> 116
atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48
Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
      1                      5                      10                      15
ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96
Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
      20                      25                      30

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tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu 35 40 45	144
aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn 50 55 60	192
ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu 65 70 75 80	240
tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr 85 90 95	288
gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser 100 105 110	336
aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His 115 120 125	384
caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile 130 135 140	432
gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe 145 150 155 160	480
aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg 165 170 175	528
tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly 180 185 190	576
agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser 195 200 205	624
aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val 210 215 220	672
att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn 225 230 235 240	720
gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln 245 250 255	768
atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly 260 265 270	816
ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile 275 280 285	864

gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr	912
290 295 300	
gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His	960
305 310 315 320	
caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile	1008
325 330 335	
agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile	1056
340 345 350	
gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser	1104
355 360 365	
gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly	1152
370 375 380	
aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu	1200
385 390 395 400	
ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu	1248
405 410 415	
gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val	1296
420 425 430	
aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala	1344
435 440 445	
agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu	1392
450 455 460	
ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gln	1440
465 470 475 480	
aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile	1488
485 490 495	
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu	1536
500 505 510	
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser	1584
515 520 525	
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly	1632
530 535 540	

aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga 1680
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
 545 550 555 560
 aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat 1728
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
 565 570 575
 gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg 1776
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
 580 585 590
 atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct 1824
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
 595 600 605
 caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc 1872
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
 610 615 620
 ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga 1920
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
 625 630 635 640
 gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat 1968
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
 645 650 655
 tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta 2016
 Ser Glu Gly Ala Met Asn Leu Thr Tyr Ala Asp Arg Thr Val Tyr Asn Leu
 660 665 670
 ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta 2064
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
 675 680 685
 att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa 2112
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
 690 695 700
 aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt 2160
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
 705 710 715 720
 tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg 2204
 Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
 725 730

<210> 117

<211> 734

<212> PRT

<213> Pasteurella multocida

<400> 117

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1 5 10 15
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
 20 25 30
 Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
 35 40 45

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Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
  50                      55                      60
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
  65                      70                      75                      80
Leu Leu Ser Val Val Gln Arg Lys Pro Leu Met Ala Gln Ala Ser Asp Thr
                      85                      90                      95
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
  100                      105                      110
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
  115                      120                      125
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
  130                      135                      140
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
  145                      150                      155                      160
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
                      165                      170                      175
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
                      180                      185                      190
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
                      195                      200                      205
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
  210                      215                      220
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
  225                      230                      235                      240
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
                      245                      250                      255
Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
                      260                      265                      270
Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
                      275                      280                      285
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
                      290                      295                      300
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
  305                      310                      315                      320
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
                      325                      330                      335
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
                      340                      345                      350
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
                      355                      360                      365
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
                      370                      375                      380

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Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
 385 390 395 400
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
 405 410 415
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
 420 425 430
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
 435 440 445
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
 450 455 460
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
 465 470 475 480
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
 485 490 495
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
 500 505 510
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
 515 520 525
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
 530 535 540
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
 545 550 555 560
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
 565 570 575
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
 580 585 590
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
 595 600 605
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
 610 615 620
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
 625 630 635 640
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
 645 650 655
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
 660 665 670
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
 675 680 685
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
 690 695 700
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
725 730

<210> 118
<211> 251
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> unkO

<220>
<221> CDS
<222> (1)..(249)

<400> 118
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
1 5 10 15
gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30
tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45
gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
50 55 60
agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65 70 75 80
tgt aat cat ta 251
Cys Asn His

<210> 119
<211> 83
<212> PRT
<213> *Pasteurella multocida*

<400> 119
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
1 5 10 15
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
50 55 60
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65 70 75 80

Cys Asn His

<210> 120

<211> 548

<212> DNA

<213> *Pasteurella multocida*

<220>

<223> unkP

<220>

<221> CDS

<222> (1)..(546)

<400> 120

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atg cgt gca tat ctt gat aaa gaa cag gcc tgg cat acg tct att tca 48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15

aat aaa gcc att aat gcc gtg agc ggt gtc aca caa cca ctc tat ttt 96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30

gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa gcc 144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

atc acg tgt tgc gtg aat cat aat gcc ttt cgt ttt tgg gcc tta cgc 192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg 288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

aat gcg aag tgg cgt gat tac acc aca aaa gcc tac tta att gcc ggt 384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat 432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa 480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

cag cta gcc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt 528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

tca aat cgt tta gca tcg ta 548

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Ser Asn Arg Leu Ala Ser
180

<210> 121

<211> 182

<212> PRT

<213> *Pasteurella multocida*

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15

Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30

Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

Ser Asn Arg Leu Ala Ser
180

<210> 122

<211> 69

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> apvA-or1

<220>

<221> CDS

<222> (1)..(69)

<400> 122

atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

gat aag ttt aag ata ctt agc
 Asp Lys Phe Lys Ile Leu Ser
 20

69

<210> 123
 <211> 23
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 123
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
 1 5 10 15

Asp Lys Phe Lys Ile Leu Ser
 20

<210> 124
 <211> 64
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvA-or2

<220>
 <221> CDS
 <222> (3)..(62)

<400> 124
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
 1 5 10 15

ttg gca agc atg aca ta 64
 Leu Ala Ser Met Thr
 20

<210> 125
 <211> 20
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 125
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
 1 5 10 15

Ala Ser Met Thr
 20

<210> 126
 <211> 653
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvB

<220>
 <221> CDS

<222> (1)..(651)

<400> 126

tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48
 Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1 5 10 15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa 96
 Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
 20 25 30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144
 His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Ser Gly
 35 40 45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192
 Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
 50 55 60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240
 Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65 70 75 80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288
 Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
 85 90 95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336
 Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
 100 105 110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384
 Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
 115 120 125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432
 Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
 130 135 140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480
 Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
 145 150 155 160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528
 Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
 165 170 175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576
 Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
 180 185 190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624
 Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
 195 200 205

ctt ggc atg ggt tta tct gtc ggt tgg at 653
 Leu Gly Met Gly Leu Ser Val Gly Trp
 210 215

<210> 127

<211> 217

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

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Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1             5             10             15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
          20             25             30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
          35             40             45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
          50             55             60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
          65             70             75             80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
          85             90             95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
          100            105            110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
          115            120            125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
          130            135            140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
          145            150            155            160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
          165            170            175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
          180            185            190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
          195            200            205

Leu Gly Met Gly Leu Ser Val Gly Trp
          210            215

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<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1) .. (240)

<400> 128

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atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat   48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1             5             10             15

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atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Ile Ala Lys Glu
20 25 30

ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
35 40 45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
50 55 60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65 70 75 80

at 242

<210> 129
<211> 80
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
1 5 10 15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
20 25 30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
35 40 45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
50 55 60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
65 70 75 80

<210> 130
<211> 527
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvD

<220>
<221> CDS
<222> (1)..(525)

<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
1 5 10 15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
20 25 30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
 35 40 45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
 50 55 60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
 65 70 75 80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
 85 90 95

aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
 100 105 110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 131

<211> 175

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 131

Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1 5 10 15

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
 20 25 30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
 35 40 45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
 50 55 60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
 65 70 75 80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
 85 90 95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
 100 105 110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 132
 <211> 867
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> atpG

<220>
 <221> CDS
 <222> (1) .. (864)

<400> 132
 atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1 5 10 15
 act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
 20 25 30
 cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
 35 40 45
 atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
 50 55 60
 cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
 65 70 75 80
 gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95
 aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336
 Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
 100 105 110
 gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
 115 120 125
 cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
 130 135 140
 gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
 145 150 155 160
 cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa 528
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
 165 170 175
 aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
 180 185 190
 aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624
 Lys Leu Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
 195 200 205
 tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
 210 215 220
 tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa 720
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
 225 230 235 240
 caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt 768
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255
 aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca 816
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270
 agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att 864
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285
 taa 867

 <210> 133
 <211> 288
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

 <400> 133
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1 5 10 15
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
 20 25 30
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
 35 40 45

 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
 50 55 60
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
 65 70 75 80
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
 100 105 110
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
 115 120 125
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
 130 135 140
 Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
 145 150 155 160
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
 165 170 175
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
 180 185 190
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
 195 200 205
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
 210 215 220
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
 225 230 235 240
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 134
 <211> 534
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> atpH

<220>
 <221> CDS
 <222> (1)..(531)

<400> 134
 atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
 20 25 30
 cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
 35 40 45
 aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192

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Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60
tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg   240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80
gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc   288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
  85                      90                      95
gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt   336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
  100                     105                     110
tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg   384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
  115                     120                     125
atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat   432
Met Glu Lys Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
  130                     135                     140
aac agc ctg att gca gcg gta att att aaa tac gat gat gtt gtt att   480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
  145                     150                     155                     160
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc   528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
  165                     170                     175
ttg taa
Leu
534

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<210> 135

<211> 177

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 135

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Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
  1                      5                      10                     15

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Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
  20                     25                     30

```

```

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
  35                     40                     45

```

```

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60

```

```

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80

```

```

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
  85                      90                      95

```

```

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
  100                     105                     110

```



```

Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
    115                      120                      125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
    130                      135                      140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
    145                      150                      155                      160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
    165                      170                      175

Leu

```

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<210> 136
<211> 321
<212> DNA
<213> Actinobacillus pleuropneumoniae

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<220>
<223> dksA

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<220>
<221> CDS
<222> (1)..(318)

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<400> 136
gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa   48
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
    1                      5                      10                      15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act   96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
    20                      25                      30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt   144
Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
    35                      40                      45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac   192
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
    50                      55                      60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt   240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
    65                      70                      75                      80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt   288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
    85                      90                      95

gcg gaa atc cgt gaa aag caa atg ggc tta taa   321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
    100                      105

```

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<210> 137
<211> 106
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<400> 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 138

<211> 33

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dnaK

<220>

<221> CDS

<222> (1) .. (30)

<400> 138

gct gag ttt gaa gaa gtg aaa gat aat aaa taa
 Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

33

<210> 139

<211> 10

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 140

<211> 453

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> exbB

<220>

<221> CDS

<222> (1) .. (450)

<400> 140
 atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
 Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
 20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
 Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
 35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
 Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
 50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
 Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
 65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
 Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
 85 90 95

gac gcc gca tcc att atg gtt cac ctt tgc ctt gca tta aaa gca acc 336
 Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
 100 105 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384
 Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
 115 120 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432
 Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
 130 135 140

gct cgt aaa gcc aat caa taa 453
 Ala Arg Lys Ala Asn Gln
 145 150

<210> 141

<211> 150

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 141

Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
 20 25 30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
 35 40 45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
 50 55 60

Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
 65 70 75 80

Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
85 90 95
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
100 105 110
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
115 120 125
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
130 135 140
Ala Arg Lys Ala Asn Gln
145 150

<210> 142

<211> 720

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> fkpA

<220>

<221> CDS

<222> (1)..(717)

<400> 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
1 5 10 15

ggt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
35 40 45

ggt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
 165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
 180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
 195 200 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa 672
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
 210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
 225 230 235

<210> 143
 <211> 239
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 143
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
 1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
 20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
 35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
 50 55 60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
 65 70 75 80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
 85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
 100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
 115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
 130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
 145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
 165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
 180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
 195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
 210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
 225 230 235

<210> 144

<211> 290

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> HI0379

<220>

<221> CDS

<222> (3) .. (287)

<400> 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln
 1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn
 20 25 30

ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct 143
 Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
 35 40 45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191
 Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
 50 55 60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239
 Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
 65 70 75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287
 Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
 80 85 90 95

taa 290

<210> 145

<211> 95

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 145

His Ser Val Arg Gly Pro Gly Gly Tyr Gln Leu Gly Lys Gln Pro

1	5	10	15
Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu	20	25	30
Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln	35	40	45
Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val	50	55	60
Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp	65	70	75
His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	85	90	95

<210> 146

<211> 273

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> hupA

<220>

<221> CDS

<222> (1)..(270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	
agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc	96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	
tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt	144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	
act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt	192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	
acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt	240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	
gca ggt aaa gca tta aaa gat tta gta aaa taa	273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 147

<211> 90

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu

1	5	10	15
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	20	25	30
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	35	40	45
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	50	55	60
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	65	70	75
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	85	90	

<210> 148

<211> 551

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> lpdA

<220>

<221> CDS

<222> (1)..(549)

<400> 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct	48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Leu Gly Ala Gly Pro	
1 5 10 15	
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca	96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr	
20 25 30	
gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta	144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val	
35 40 45	
ggg tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa	192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu	
50 55 60	
gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac	240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn	
65 70 75 80	
att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa	288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys	
85 90 95	
tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta	336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val	
100 105 110	
gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt	384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg	
115 120 125	

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
 130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175

gaa aaa att act cat tat ggg cc 551
 Glu Lys Ile Thr His Tyr Gly
 180

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro
 1 5 10 15

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
 20 25 30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
 35 40 45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
 50 55 60

Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
 65 70 75 80

Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
 85 90 95

Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
 100 105 110

Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
 115 120 125

Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
 130 135 140

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160

Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175

Glu Lys Ile Thr His Tyr Gly
 180

<210> 150

<211> 1095

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1) .. (1092)

<400> 150

atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta	48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val	
1 5 10 15	
gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca	96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala	
20 25 30	
ggg tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa	144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys	
35 40 45	
aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act	192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr	
50 55 60	
tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt	240
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly	
65 70 75 80	
tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct	288
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser	
85 90 95	
gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca	336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala	
100 105 110	
cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac	384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp	
115 120 125	
tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat	432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr	
130 135 140	
aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa	480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln	
145 150 155 160	
agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa	528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu	
165 170 175	
tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca	576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala	
180 185 190	
agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat	624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp	
195 200 205	

atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg 672
 ile ser ser val ser ala gly leu ser tyr arg phe gly gln gly ala
 210 215 220

gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc 720
 ala pro val ala ala pro ala val glu thr lys asn phe ala phe ser
 225 230 235 240

tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg 768
 ser asp val leu phe ala phe gly lys ser asn leu lys pro ala ala
 245 250 255

gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta 816
 ala thr ala leu asp ala met gln thr glu ile asn asn ala gly leu
 260 265 270

tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa 864
 ser asn ala ala ile gln val asn gly tyr thr asp arg ile gly lys
 275 280 285

gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct 912
 glu ala ser asn leu lys leu ser gln arg arg ala glu thr val ala
 290 295 300

aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta 960
 asn tyr ile val ser lys gly ala pro ala ala asn val thr ala val
 305 310 315 320

ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008
 gly tyr gly glu ala asn pro val thr gly ala thr cys asp lys val
 325 330 335

aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056
 lys gly arg lys ala leu ile ala cys leu ala pro asp arg arg val
 340 345 350

gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa 1095
 glu val gln val gln gly thr lys glu val thr met
 355 360

<210> 151
 <211> 364
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 151
 Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
 1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
 20 25 30

Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
 35 40 45

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
 50 55 60

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
 65 70 75 80

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser

85										90										95																																		
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala																																							
			100						105					110																																								
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp																																							
			115					120					125																																									
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr																																							
			130				135					140																																										
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln																																							
					150					155				160																																								
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu																																							
					165				170					175																																								
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala																																							
					180				185					190																																								
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp																																							
					195			200					205																																									
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala																																							
					210			215				220																																										
Ala	Pro	Val	Ala	Ala	Pro	Ala	Val	Glu	Thr	Lys	Asn	Phe	Ala	Phe	Ser																																							
						230				235				240																																								
Ser	Asp	Val	Leu	Phe	Ala	Phe	Gly	Lys	Ser	Asn	Leu	Lys	Pro	Ala	Ala																																							
					245				250					255																																								
Ala	Thr	Ala	Leu	Asp	Ala	Met	Gln	Thr	Glu	Ile	Asn	Asn	Ala	Gly	Leu																																							
					260				265					270																																								
Ser	Asn	Ala	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Lys																																							
					275				280				285																																									
Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	Ala	Glu	Thr	Val	Ala																																							
						295						300																																										
Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val																																							
					310				315					320																																								
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val																																							
					325				330				335																																									
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val																																							
					340				345				350																																									
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met																																											
					355						360																																											

<210> 152

<211> 1110

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5

<220>

<221> CDS

<222> (1) .. (1107)

<400> 152

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atg aaa aaa tca tta gtt gct tta gca gta tta tcg gct gca gca gta 48
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
      1              5              10              15

gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt 96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
      20              25              30

ggt caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac 144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
      35              40              45

gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac 192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
      50              55              60

tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat 240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
      65              70              75

aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta 288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Asp Tyr Tyr Gly Arg Val
      85              90              95

cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt 336
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
      100             105             110

tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac 384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
      115             120             125

gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa 432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
      130             135             140

tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta 480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
      145             150             155

aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct 528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
      165             170             175

gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac 576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
      180             185             190

tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa 624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
      195             200             205

tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc 672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
      210             215             220

ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa 720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
      225             230             235

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aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc 768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
      245                                250                                255

tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc 816
Leu Lys Pro Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
      260                                265                                270

gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca 864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
      275                                280                                285

gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt 912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
      290                                295                                300

gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca 960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
      305                                310                                315                                320

aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca 1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
      325                                330                                335

aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca 1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
      340                                345                                350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct 1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
      355                                360                                365

atg taa 1110
Met

<210> 153
<211> 369
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
  1      5      10      15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
  20      25      30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
  35      40      45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
  50      55      60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
  65      70      75      80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
  85      90      95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
  100     105     110

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Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
 115 120 125
 Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
 130 135 140
 Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
 145 150 155 160
 Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
 165 170 175
 Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
 180 185 190
 Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
 195 200 205
 Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
 210 215 220
 Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
 225 230 235 240
 Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
 245 250 255
 Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
 260 265 270
 Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
 275 280 285
 Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
 290 295 300
 Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
 305 310 315 320
 Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
 325 330 335
 Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
 340 345 350
 Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
 355 360 365

Met

<210> 154

<211> 1076

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> pnp new

<220>

<221> CDS

<222> (1)..(1074)

<400> 154
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Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30

gcg gaa gcg cgt atc ggc gat ccg tat cgt att aca gaa aaa caa gcg 144
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta 192
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att 240
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80

acc gca tta gaa agt tct att gtt gcg ggt cgt att att gcc gcc gaa 288
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110

tgc acc gcc gta tta cct cgt acg cac ggt tct gca atc ttt act gcg 384
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125

ggt gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat 432
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140

gca caa att gtt gac gaa tta acc gcc gag aaa tca gac cgt ttc tta 480
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc 528
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175

ggt tcg ccg aaa cgt cgt gaa atc gcc cac ggt cgt tta gcg aaa cgc 576
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190

ggt gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg 624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205

gcg gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct 672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220

tcc gta tgc gcc gca tct tta gcg tta atg gac gca gcc gta ccg att 720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240

aaa gcg gcg gtt gcg ggt atc gca atg gcc tta gtg aaa gaa gaa gaa 768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu

245	250	255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc	816		
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly			
260	265	270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt	864		
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu			
275	280	285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc	912		
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile			
290	295	300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg	960		
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met			
305	310	315	320
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct	1008		
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro			
325	330	335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc	1056		
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile			
340	345	350	
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Gly Lys Gly Gly Ala Val			
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Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu			
20	25	30	
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala			
35	40	45	
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu			
50	55	60	
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile			
65	70	75	80
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu			
85	90	95	
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile			
100	105	110	
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg			
115	120	125	
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp			

130 135 140
 Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
 145 150 155 160
 Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
 165 170 175
 Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
 180 185 190
 Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
 195 200 205
 Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
 210 215 220
 Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
 225 230 235 240
 Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu
 245 250 255
 Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly
 260 265 270
 Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu
 275 280 285
 Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
 290 295 300
 Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
 305 310 315
 Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
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 Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
 340 345 350
 Gly Lys Gly Gly Ala Val
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 tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala	20	25	30	
caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat	144			
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr	35	40	45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa	192			
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys	50	55	60	
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta	240			
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu	65	70	75	80
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac	288			
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn	85	90	95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat	336			
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp	100	105	110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac	384			
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn	115	120	125	
aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt	432			
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly	130	135	140	
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc	480			
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe	145	150	155	160
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa	528			
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln	165	170	175	
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta	576			
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu	180	185	190	
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac	624			
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr	195	200	205	
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac	672			
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp	210	215	220	
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta	720			
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu	225	230	235	240
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac	768			
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn	245	250	255	
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc	816			
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala				

260	265	270	
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac	864		
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn			
275	280	285	
tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt	912		
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly			
290	295	300	
tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att	960		
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile			
305	310	315	320
acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca	1008		
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala			
325	330	335	
caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta	1055		
Gln Trp Gln Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys			
340	345	350	
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20	25	30	
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr			
35	40	45	
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys			
50	55	60	
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu			
65	70	75	80
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn			
85	90	95	
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp			
100	105	110	
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn			
115	120	125	
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly			
130	135	140	
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe			
145	150	155	160
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln			
165	170	175	
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu			

180	185	190	
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr			
195	200	205	
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp			
210	215	220	
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu			
225	230	235	240
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn			
	245	250	255
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala			
	260	265	270
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn			
	275	280	285
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly			
	290	295	300
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile			
305	310	315	320
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala			
	325	330	335
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys			
	340	345	350

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 cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn 20 25 30
 cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act 144
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr 35 40 45
 ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg 192
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr 50 55 60
 gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt 240

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
65 70 80

aca caa acg ctt gac tgt tgc ttt tgt ttc agt ccg gtg tcc aat atg 288
Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
85 90 95

gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
100 105 110

gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
115 120 125

atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
130 135 140

tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145 150 155 160

aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
165 170

<210> 159
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<212> PRT
<213> Actinobacillus pleuropneumoniae

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20 25 30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
35 40 45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
50 55 60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
65 70 75 80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
85 90 95

Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
100 105 110

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
115 120 125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
130 135 140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
145 150 155 160

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 160

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<213> Actinobacillus pleuropneumoniae

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<222> (1)..(1299)

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att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30

aaa ggc tat cgc aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45

gta cgc cac gca att atc gaa caa cgt ttc ggt tta cgc gct cgc caa 192
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60

gac gta tta tcc gat gaa atg caa cgt cgc ttc ttt gat cgc gta atc 240
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80

gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca cgc aac aac 288
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
 85 90 95

tac caa cgc agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
 100 105 110

ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa cgc 384
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
 115 120 125

gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
 130 135 140

cgt aaa caa caa cgc act tgg gct gaa tct caa gca cgc gca caa cgc 480
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
 145 150 155 160

gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
 165 170 175

ttt gaa ggc ggt aaa cgc aca gac ttc act tta gca atg ggt caa agt 576
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser

180	185	190	
cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc 624			
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly			
195	200	205	
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa 672			
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu			
210	215	220	
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta 720			
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val			
225	230	235	240
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc 768			
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe			
	245	250	255
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat 816			
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn			
	260	265	270
atg caa cgt gaa ctt aaa aac gca gta acc gca gcg gtt aaa aac caa 864			
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln			
	275	280	285
gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca 912			
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala			
	290	295	300
gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt 960			
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg			
305	310	315	320
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc 1008			
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe			
	325	330	335
gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc 1056			
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr			
	340	345	350
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa 1104			
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu			
	355	360	365
acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt 1152			
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val			
	370	375	380
gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta 1200			
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val			
385	390	395	400
gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta 1248			
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val			
	405	410	415
act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa 1296			
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<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 161

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Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
          35           40           45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
          50           55           60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
          65           70           75           80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
          85           90           95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
          100          105          110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
          115          120

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
          130          135          140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
          145          150          155          160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
          165          170          175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
          180          185          190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
          195          200          205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
          210          215          220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
          225          230          235          240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
          245          250          255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
          260          265          270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
          275          280          285

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Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290                295                300
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 305                310                315                320
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
                325                330                335
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
                340                345                350
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355                360                365
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370                375                380
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385                390                395                400
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
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Gly

<210> 162

<211> 316

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

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<400> 162

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tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaaac 180
tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
agctgaacaa aagcagctaa gtgtttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300
taaaatttga aaatat

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316

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<211> 85

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> tRNA-leu

<400> 163

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gagttcagat ctcgccaga gcacc

85

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<212> DNA

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<222> (1) .. (621)

<400> 164

atg	caa	gaa	ctc	aca	cct	caa	atg	tgg	ggc	tta	gtc	ggc	act	tca	acg	48
Met	Gln	Glu	Leu	Thr	Pro	Gln	Met	Trp	Gly	Leu	Val	Gly	Thr	Ser	Thr	
1					5				10					15		

ctt	gaa	acg	ctc	tat	atg	ggc	ttt	gcg	gcg	act	tta	ctt	gct	gtg	gta	96
Leu	Glu	Thr	Leu	Tyr	Met	Gly	Phe	Ala	Ala	Thr	Leu	Leu	Ala	Val	Val	
			20					25					30			

gtc	ggt	ttg	ccg	atc	ggt	ttt	ctg	gca	ttt	tta	acc	ggt	aaa	gga	gag	144
Val	Gly	Leu	Pro	Ile	Gly	Phe	Leu	Ala	Phe	Leu	Thr	Gly	Lys	Gly	Glu	
		35					40					45				

att	tta	gag	aat	ccg	cgt	tta	cat	caa	gta	tta	gat	gtg	att	att	aat	192
Ile	Leu	Glu	Asn	Pro	Arg	Leu	His	Gln	Val	Leu	Asp	Val	Ile	Ile	Asn	
		50				55					60					

atc	ggt	cgt	tcc	gta	ccg	ttt	att	att	ttg	tta	gtc	gtg	ttg	tta	cct	240
Ile	Gly	Arg	Ser	Val	Pro	Phe	Ile	Ile	Leu	Val	Val	Val	Leu	Leu	Pro	
		65			70					75					80	

ttt	acg	cgt	tta	ttg	gtc	ggg	aca	acg	ctc	ggt	act	acg	gcg	gcg	att	288
Phe	Thr	Arg	Leu	Leu	Val	Gly	Thr	Thr	Leu	Gly	Thr	Thr	Ala	Ala	Ile	
			85						90					95		

gtg	ccg	tta	agc	ggt	tcg	gca	att	ccg	ttt	ttt	gcg	cgt	tta	act	tca	336
Val	Pro	Leu	Ser	Val	Ser	Ala	Ile	Pro	Phe	Phe	Ala	Arg	Leu	Thr	Ser	
		100						105					110			

aat	gcg	tta	tta	gaa	atc	cca	gca	ggt	tta	acc	gaa	gcg	gcg	aaa	tcg	384
Asn	Ala	Leu	Leu	Glu	Ile	Pro	Ala	Gly	Leu	Thr	Glu	Ala	Lys	Ser		
		115					120					125				

atg	ggc	gca	acg	aat	tgg	caa	gtg	gtc	agt	aaa	ttt	tat	tta	ccg	gaa	432
Met	Gly	Ala	Thr	Asn	Trp	Gln	Val	Val	Ser	Lys	Phe	Tyr	Leu	Pro	Glu	
		130				135					140					

tca	ctg	ccg	att	tta	atc	aat	ggt	atc	aca	tta	act	tta	gtc	gct	tta	480
Ser	Leu	Pro	Ile	Leu	Ile	Asn	Gly	Ile	Thr	Leu	Thr	Leu	Val	Ala	Leu	
		145			150					155				160		

atc	ggt	tat	tcg	gca	atg	gcg	ggt	gcg	gtc	ggc	ggc	ggc	ggt	ttg	ggg	528
Ile	Gly	Tyr	Ser	Ala	Met	Ala	Gly	Ala	Val	Gly	Gly	Gly	Gly	Leu	Gly	
			165					170						175		

aac	ctt	gcc	atc	agt	tac	ggt	gaa	cac	cga	aat	atg	gtc	tat	gta	aaa	576
Asn	Leu	Ala	Ile	Ser	Tyr	Gly	Glu	His	Arg	Asn	Met	Val	Tyr	Val	Lys	
		180						185						190		

tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa 623
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
 195 200 205

<210> 165
 <211> 207
 <212> PRT
 <213> *Actinobacillus pleuropneumoniae*

<400> 165
 Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
 1 5 10 15
 Leu Glu Thr Leu Tyr Met Gly Phe Ala Thr Leu Leu Ala Val Val
 20 25 30
 Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
 35 40 45
 Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
 50 55 60
 Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
 65 70 75 80
 Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
 85 90 95
 Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
 100 105 110
 Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Lys Ser
 115 120 125
 Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
 130 135 140
 Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
 145 150 155 160
 Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
 165 170 175
 Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
 180 185 190
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
 195 200 205

<210> 166
 <211> 866
 <212> DNA
 <213> *Pasteurella (Mannheimia) haemolytica*

<220>
 <221> CDS
 <222> (1)..(864)
 <220>
 <223> atpG

<400> 166
 atg gca ggt gct aaa gag ata aga acc aaa att gca agt gtt cgt aat 48
 Met Ala Gly Ala Lys 5 Glu Ile Arg Thr Lys 10 Ile Ala Ser Val Arg Asn 15
 1

aca caa aaa att acc aaa gcg atg gaa atg gtt gcc gca tca aaa atg 96
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met 20 25 30

cgt aaa acc caa gag cgt atg gcg gct tct cgc cct tat gct gaa agt 144
 Arg Lys 35 Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser 40 45

att cgc aag gca att agc cat att gcc aaa ggt aac att gag tat aaa 192
 Ile Arg Lys Ala Ile Ser His 55 Ile Ala Lys Gly Asn Ile Glu Tyr Lys 50 60

cac cca ttt ttg acc cca cgt ccg gta aaa aaa gtt gcc tat tta gta 240
 His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val 65 70 75 80

gtt tca acc gat cgc ggt tta tgt ggt gcc tta aat atc aat tta ttt 288
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe 85 90 95

aaa acc gtt tta cat gaa ttg aaa gaa aaa gat gac caa ggt gtt aag 336
 Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys 100 105 110

tct cga ctt gct gtg gtg gga aat aaa ggg atc tcc ttt ttt aac cca 384
 Ser Arg Leu Ala Val Val Gly Asn Lys Lys Gly Ile Ser Phe Phe Asn Pro 115 120 125

atg ggg cta gag att aaa ggt cat atc aat gga ttg ggt gat aca ccg 432
 Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro 130 135 140

gca atg gaa gat tta gtc ggt att gtt aat ggt atg gta aat gcc tac 480
 Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr 145 150 155 160

cgt gaa gcc gaa att gat gaa gtg tat gtg gta tat aac cgt ttt ata 528
 Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile 165 170 175

aac acg atg tca caa aaa ccg aca gta caa cag ttg ctt cct ttg cct 576
 Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro 180 185 190

gca ctg gaa aat gac tca tta gag caa act ggt tct tgg gat tat ctc 624
 Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu 195 200 205

tat gaa cca aat cca caa gcg tta tta gac agc tta ctg gtt cgt tat 672
 Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr 210 215 220

tta gaa tct caa gtt tat cag gca gtg gta gat aat ctt gcg tct gaa 720
 Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu 225 230 235 240

cag gct gct cga atg gtg gca atg aaa gca gca acc gat aac gca ggt 768
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly

	245	250	255	
aat ctg att	aat gag tta	cag tta gtg	tat aac aaa gct	cgt caa gca 816
Asn Leu Ile	Asn Glu Leu	Gln Leu Val	Tyr Asn Lys Ala	Arg Gln Ala
	260	265	270	
agt att acg	aat gaa tta	aat gaa att	gtc gcg ggt gcc	gca gca att 864
Ser Ile Thr	Asn Glu Leu	Asn Glu Ile	Val Ala Gly Ala	Ala Ala Ile
	275	280	285	
ta				866
<210> 167				
<211> 288				
<212> PRT				
<213> Pasteurella (Mannheimia) haemolytica				
<400> 167				
Met Ala Gly	Ala Lys Glu	Ile Arg Thr	Lys Ile Ala	Ser Val Arg Asn
1	5	10	15	
Thr Gln Lys	Ile Thr Lys	Ala Met Glu	Met Val Ala	Ala Ser Lys Met
	20	25	30	
Arg Lys Thr	Gln Glu Arg	Met Ala Ala	Ser Arg Pro	Tyr Ala Glu Ser
	35	40	45	
Ile Arg Lys	Ala Ile Ser	His Ile Ala	Lys Gly Asn	Ile Glu Tyr Lys
	50	55	60	
His Pro Phe	Leu Thr Pro	Arg Pro Val	Lys Lys Val	Gly Tyr Leu Val
	65	70	75	80
Val Ser Thr	Asp Arg Gly	Leu Cys Gly	Gly Leu Asn	Ile Asn Leu Phe
	85	90	95	
Lys Thr Val	Leu His Glu	Leu Lys Glu	Lys Asp Asp	Gln Gly Val Lys
	100	105	110	
Ser Arg Leu	Ala Val Val	Gly Asn Lys	Gly Ile Ser	Phe Phe Asn Pro
	115	120	125	
Met Gly Leu	Glu Ile Lys	Gly His Ile	Asn Gly Leu	Gly Asp Thr Pro
	130	135	140	
Ala Met Glu	Asp Leu Val	Gly Ile Val	Asn Gly Met	Val Asn Ala Tyr
	145	150	155	160
Arg Glu Gly	Glu Ile Asp	Glu Val Tyr	Val Val Tyr	Asn Arg Phe Ile
	165	170	175	
Asn Thr Met	Ser Gln Lys	Pro Thr Val	Gln Gln Leu	Leu Pro Leu Pro
	180	185	190	
Ala Leu Glu	Asn Asp Ser	Leu Glu Gln	Thr Gly Ser	Trp Asp Tyr Leu
	195	200	205	
Tyr Glu Pro	Asn Pro Gln	Ala Leu Leu	Asp Ser Leu	Leu Val Arg Tyr
	210	215	220	
Leu Glu Ser	Gln Val Tyr	Gln Ala Val	Val Asp Asn	Leu Ala Ser Glu
	225	230	235	240

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255

Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 168

<211> 1463

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> guaB

<400> 168

atg cta cga att aaa caa gaa gcc ctc act ttt gat gat gtt ctt ctc 48
 Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu
 1 5 10 15

gtc ccg gca cat tct act gtg ctt cct aat act gct gat ctt tct act 96
 Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
 20 25 30

caa tta act aaa acc att cgt tta aac att ccg atg ctt tct gct gca 144
 Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
 35 40 45

atg gat acc gtt aca gaa act aag ctt gcg atc tcc ctt gct caa gaa 192
 Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50 55 60

ggc gcc att ggt ttt atc cat aaa aat atg tcg att gaa cgc cag gca 240
 Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65 70 75 80

gac cgt gtg cgt aaa gtg aaa aaa ttt gaa agt ggt att gtt tct gag 288
 Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu
 85 90 95

cca gtg acg att tct cct gat atg aca tta gcg gaa ttg gct gaa ttg 336
 Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu
 100 105 110

gtg aaa aag aac ggt ttt gca gcc tat ccg gtg att gat gaa aac caa 384
 Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln
 115 120 125

aat tta gtg gga att att acc gga cgt gat acc cga ttt gtc acg gat 432
 Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
 130 135 140

tta agc aaa aca gtg cgt gaa ttt atg aca cca aaa gac cgt tta gtg 480
 Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val
 145 150 155 160

acg gta aaa gaa aac gca agc cgt gaa gaa att ttc cac tta atg cac	528
Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His	
165 170 175	
gaa cac cga gtg gag aaa gtg ctg gta gtg aat aat gaa ttt cag tta	576
Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu	
180 185 190	
aaa gga atg att acc cta aaa gac tac caa aaa gcg gaa agc aaa ccg	624
Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro	
195 200 205	
aat gcc tgt aaa gat gag ttt ggg cgt ttg cgt gtg ggg gcg gca gtg	672
Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val	
210 215 220	
gga gcc ggt ccg ggc aat gaa gaa cga att gat gct tta gta aaa gcg	720
Gly Ala Gly Pro Glu Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala	
225 230 235 240	
ggg gtc gat gtg cta tta atc gac tct tcg cac ggg cat tct gaa ggt	768
Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly	
245 250 255	
gta tta caa cgt gtg cgt gaa acc cgt gca aaa tac cct gat tta ccg	816
Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro	
260 265 270	
att gtt gcc ggt aat att gcc act gca gaa gga gcg att gcg tta gct	864
Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala	
275 280 285	
gat gca gga gcc agt gct gtg aaa gta gga atc ggc ccg ggt tca att	912
Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile	
290 295 300	
tgt acc acc aga att gta aca ggc gtt ggc gtg cca caa atc acg gca	960
Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala	
305 310 315 320	
atc gca gaa gcg gca gct gcg ctt aaa gaa cga ggc att cct gtg att	1008
Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile	
325 330 335	
gct gat ggt gga att cgt tat tca ggc gat att tca aaa gct att gcc	1056
Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala	
340 345 350	
gcc ggt gca agt tgc gta atg gtc ggt tcg atg ttt gcc ggc aca gaa	1104
Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu	
355 360 365	
gaa gcc ccg ggt gaa att gag ctt tat caa ggc aga gca ttc aaa tcc	1152
Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser	
370 375 380	
tac cgt gga atg gga tca tta ggt gca atg agt aaa ggc tcg tca gat	1200
Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Lys Gly Ser Ser Asp	
385 390 395 400	
gcg tat ttc caa tct gat aat gcc gcc gac aag ctc gta ccg gaa ggg	1248
Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly	
405 410 415	

att gaa ggg cgt atc gct tac aaa ggc tac ttg aaa gaa att atc cac 1296
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His
 420 425 430

caa caa atg ggc ggc tta cgc tcc tgt atg gga tta acc ggc tgt gcc 1344
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445

act att gaa gaa ctc cgc acc aaa gca gaa ttt gtc cgc att agt ggt 1392
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly
 450 455 460

gct ggt att aaa gaa agc cac gtc cac gat gtg aca att acc aaa gaa 1440
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
 465 470 475 480

gca ccg aac tac cga atg ggt ta 1463
 Ala Pro Asn Tyr Arg Met Gly
 485

<210> 169

<211> 487

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 169

Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu
 1 5 10 15

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
 20 25 30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
 35 40 45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50 55 60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65 70 75 80

Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu
 85 90 95

Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu
 100 105 110

Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln
 115 120 125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
 130 135 140

Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val
 145 150 155 160

Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His
 165 170 175

Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu
 180 185 190

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro
 195 200 205
 Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
 210 215 220
 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
 225 230 235 240
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
 245 250 255
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
 260 265 270
 Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
 275 280 285
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
 290 295 300
 Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320
 Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile
 325 330 335
 Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly
 450 455 460
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
 465 470 475 480
 Ala Pro Asn Tyr Arg Met Gly
 485

<210> 170

<211> 2150

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

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<220>
<221> CDS
<222> (1) .. (2148)

<220>
<223> pnp

<400> 170
atg act cca att gta aaa cag ttt aaa tac ggt cag cac acc gtg acc 48
Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gln His Thr Val Thr
1 5 10 15

tta gaa acc ggt gct atc gca cgc caa gca acg gca gca gta atg gca 96
Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Val Met Ala
20 25 30

agt atg gac gac aca acc gta ttt gtt acc gta gta gcg aaa aaa gac 144
Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp
35 40 45

gta aaa gaa ggg caa gat ttc ttc cca tta acc gta gat tat caa gag 192
Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu
50 55 60

cgt act tac gca gcc ggt cgt att ccg ggc ggt ttc ttc aaa cgt gaa 240
Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Phe Phe Lys Arg Glu
65 70 75 80

gga cgt cct agc gaa ggt gaa acc tta atc gct cgc ttg atc gac cgt 288
Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg
85 90 95

cct gtg cgt cca ctt ttc cca gaa ggt ttc ttt aac gaa att caa gtg 336
Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val
100 105 110

att gcg acc gta gta tcg gta aac cca caa atc agt cct gat ctg gtt 384
Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val
115 120 125

gcg atg atc ggt gca tcg gct gcc ctt tca tta tcc ggc gtg ccg ttt 432
Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe
130 135 140

aac ggt cca atc ggt gcg gct cgt gtc ggt ttt atc aac gat caa ttc 480
Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe
145 150 155 160

gta tta aac cca acc acc agc gag caa aaa atc agc cgc tta gat tta 528
Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu
165 170 175

gtg gtt tca ggt aca gac aaa gcc gtg ttg atg gtg gaa tct gaa gcg 576
Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala
180 185 190

gat atc tta acc gaa gag caa atg tta gcg gcg gtg gtg ttc ggc cac 624
Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His
195 200 205

gag caa caa cag gtt gta atc gaa aac atc aaa gaa ttt gtt aaa gaa 672
Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu
210 215 220

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gcg ggc aaa cca cgt tgg gat tgg gtt gca cca gag cca aat aca gat Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp 225 230 235 240	720
tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala 245 250 255	768
tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile 260 265 270	816
aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser 275 280 285	864
gaa ggg act atc atc gac atc atc acc gca tta gag agc caa atc gtg Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val 290 295 300	912
cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val 305 310 315 320	960
gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr 325 330 335	1008
cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val 340 345 350	1056
gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr 355 360 365	1104
ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr 370 375 380	1152
tct gtg ggc gaa acc ggt cgt atc ggc tcg cca aaa cgc cgt gaa atc Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile 385 390 395 400	1200
ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr 405 410 415	1248
gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu 420 425 430	1296
tct aac ggt tct tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala 435 440 445	1344
ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala 450 455 460	1392
atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile 465 470 475 480	1440

tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly	1488
485 490 495	
acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly	1536
500 505 510	
atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Ala Lys Gly Ala	1584
515 520 525	
aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg	1632
530 535 540	
gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp	1680
545 550 555 560	
ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Ala Thr Ile Arg	1728
565 570 575	
gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Gly	1776
580 585 590	
acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Val Met	1824
595 600 605	
gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr	1872
610 615 620	
aac ggt aaa gta acc cgt gtg gtg gac ttc ggt gca ttc gtt tcc atc Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile	1920
625 630 635 640	
tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu	1968
645 650 655	
cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln	2016
660 665 670	
gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met	2064
675 680 685	
aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala	2112
690 695 700	
gaa aat gtg gta gaa aca gaa caa gaa aat aat ttc ta Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe	2150
705 710 715	

<210> 171

<211> 716

<212> PRT

<213> *Pasteurella (Mannheimia) haemolytica*

<400> 171

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Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr
 1           5           10           15

Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala
      20           25           30

Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp
 35           40           45

Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu
 50           55           60

Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu
 65           70           75           80

Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg
      85           90           95

Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val
 100           105           110

Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val
 115           120           125

Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe
 130           135           140

Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe
 145           150           155           160

Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu
 165           170           175

Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala
 180           185           190

Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His
 195           200           205

Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu
 210           215           220

Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp
 225           230           235           240

Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala
 245           250           255

Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile
 260           265           270

Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser
 275           280           285

Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val
 290           295           300

Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val
 305           310           315           320

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Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr
 325 330 335
 His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val
 340 345 350
 Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr
 355 360 365
 Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr
 370 375 380
 Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile
 385 390 395 400
 Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr
 405 410 415
 Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu
 420 425 430
 Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala
 435 440 445
 Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala
 450 455 460
 Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile
 465 470 475 480
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly
 485 490 495
 Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly
 500 505 510
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala
 515 520 525
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg
 530 535 540
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp
 545 550 555 560
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg
 565 570 575
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Gly
 580 585 590
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met
 595 600 605
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr
 610 615 620
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile
 625 630 635 640
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu
 645 650 655

Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln
 660 665 670
 Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met
 675 680 685
 Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Thr Val Ala
 690 695 700
 Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe
 705 710 715

<210> 172
 <211> 1517
 <212> DNA
 <213> Pasteurella (Mannheimia) haemolytica

<220>
 <221> CDS
 <222> (1)..(1515)

<220>
 <223> purF

<400> 172
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 Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala
 1 5 10 15
 att tat gat ggt tta aca tta ctt caa cac cga gga caa gat gcc gca 96
 Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30
 ggt atc gtc acc ata gac gat gaa aat cgt ttc cgc tta cgc aaa gct 144
 Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45
 aac ggc tta gtc agc gat gtt ttc cag caa gag cat atg gtg aga tta 192
 Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu
 50 55 60
 caa ggc aat gtt gga att ggt cac gtt cgc tac cca aca gca ggt agc 240
 Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80
 tca agt gtg tct gaa gcc cag cca ttt tat gtc aat tca cct ttc ggt 288
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly
 85 90 95
 att acc tta gtt cac aac ggt aat tta act aat aat gcg gaa ctt aaa 336
 Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys
 100 105 110
 gct cgc tta tac aac gaa gcc cgc cgc cat gtg aac act aat tct gat 384
 Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125
 tct gaa tcc ctt ctt aat att ttt gct tac ttt tta gat ctc tat tcc 432
 Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser
 130 135 140
 act cag cat tta agc cca gac aat atc ttt gaa acg gtt cgt aaa acc 480

Thr	Gln	His	Leu	Ser	Pro	Asp	Asn	Ile	Phe	Glu	Thr	Val	Arg	Lys	Thr	
145					150					155					160	
aat	gat	agc	att	cgt	ggc	gct	tat	gct	tgc	att	gcg	atg	att	atc	gga	528
Asn	Asp	Ser	Ile	Arg	Gly	Ala	Tyr	Ala	Cys	Ile	Ala	Met	Ile	Ile	Gly	
				165					170					175		
cac	ggc	atg	gtt	gct	ttc	cgt	gac	cca	ttc	ggc	att	gcg	ccg	tta	gtg	576
His	Gly	Met		180	Phe	Arg	Asp	Pro	Phe	Gly	Ile	Arg	Pro	Leu	Val	
								185					190			
ctg	ggc	aaa	cgt	gaa	atc	gag	ggc	aaa	acc	gaa	tat	atg	ttt	gct	tcg	624
Leu	Gly	Lys	Arg	Glu	Ile	Glu	Gly	Lys	Thr	Glu	Tyr	Met	Phe	Ala	Ser	
		195				200						205				
gaa	agt	gtg	gct	ctt	gat	gta	gtg	ggg	ttt	gaa	ttt	gtg	cga	gat	gtg	672
Glu	Ser	Val	Ala	Leu	Asp	Val	Val	Gly	Phe	Glu	Phe	Val	Arg	Asp	Val	
		210				215					220					
ctg	ccg	ggc	gaa	gcg	att	tat	gtt	acc	ttt	gat	ggg	caa	tta	cat	tcg	720
Leu	Pro	Gly	Glu	Ala	Ile	Tyr	Val	Thr	Phe	Asp	Gly	Gln	Leu	His	Ser	
		225			230				235					240		
caa	att	tgt	gcc	gat	aat	cca	aaa	ctg	aat	cct	tgt	att	ttt	gaa	tat	768
Gln	Ile	Cys	Ala	Asp	Asn	Pro	Lys	Leu	Asn	Pro	Cys	Ile	Phe	Glu	Tyr	
			245						250					255		
gtt	tat	ttt	gcc	cgt	cct	gat	tcc	gtc	att	gat	ggc	gtt	tct	gta	tat	816
Val	Tyr	Phe	Ala	Arg	Pro	Asp	Ser	Val	Ile	Asp	Gly	Val	Ser	Val	Tyr	
			260					265					270			
tct	gca	cga	gtg	cat	atg	ggc	gaa	tta	tta	ggc	gag	aaa	att	aaa	cgt	864
Ser	Ala	Arg	Val	His	Met	Gly	Glu	Leu	Leu	Gly	Glu	Lys	Ile	Lys	Arg	
		275				280						285				
gaa	tggt	gga	cga	att	atc	gat	gat	att	gat	gtg	gtg	atc	ccg	att	cct	912
Glu	Trp	Gly	Arg	Ile	Ile	Asp	Asp	Ile	Asp	Val	Val	Ile	Pro	Ile	Pro	
		290				295				300						
gaa	acc	tca	aat	gat	att	gcg	gta	cgt	att	gct	aat	atg	ttg	tat	aaa	960
Glu	Thr	Ser	Asn	Asp	Ile	Ala	Val	Arg	Ile	Ala	Asn	Met	Leu	Tyr	Lys	
		305			310					315				320		
ccc	tat	cgt	caa	ggg	ttt	gtt	aaa	aac	cgc	tat	gta	gct	cga	act	ttt	1008
Pro	Tyr	Arg	Gln	Gly	Phe	Val	Lys	Asn	Arg	Tyr	Val	Ala	Arg	Thr	Phe	
			325						330					335		
att	atg	ccg	ggg	caa	gca	cag	cgt	aaa	agc	tcg	gtt	cgc	cgt	aaa	tta	1056
Ile	Met	Pro	Gly	Gln	Ala	Gln	Arg	Lys	Ser	Ser	Val	Arg	Arg	Lys	Leu	
			340					345					350			
aat	gcg	att	gcc	tct	gaa	ttt	aaa	ggc	aaa	agc	gtg	tta	ctg	gtt	gat	1104
Asn	Ala	Ile	Ala	Ser	Glu	Phe	Lys	Gly	Lys	Ser	Val	Leu	Leu	Val	Asp	
		355				360						365				
gat	tct	att	gta	cga	ggc	aca	acg	tct	gaa	caa	atc	gtg	gaa	atg	gca	1152
Asp	Ser	Ile	Val	Arg	Gly	Thr	Thr	Ser	Glu	Gln	Ile	Val	Glu	Met	Ala	
		370				375					380					
cga	gca	gct	ggc	gca	aaa	cgg	gtt	tat	ttt	gcc	tct	gcc	gca	ccg	gaa	1200
Arg	Ala	Ala	Gly	Ala	Lys	Arg	Val	Tyr	Phe	Ala	Ser	Ala	Ala	Pro	Glu	
		385			390					395				400		

att cgc tac ccg aat gtg tat ggc att gat atg ccg act tgt gaa gaa 1248
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu
 405 410 415
 tta gtg gct tat gat cgc tca gtg gaa gag gtt gca cag atg ata ggg 1296
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly
 420 425 430
 gtg gat aaa ttg att ttc caa gac ctt gaa gca ctt tat aag tct att 1344
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile
 435 440 445
 caa ctg gaa aat ccg act att cat cgc ttt gat gac tct gta ttt aca 1392
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr
 450 455 460
 gga gaa tat att aca ggt gat gta gat aaa tgc tat tta gac agt ata 1440
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile
 465 470 475 480
 gca aga tct cga aac gat aaa gca aaa gca gag gcg gca aaa caa gcc 1488
 Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
 485 490 495
 acc aat tta gaa att cat aac gaa aga ta 1517
 Thr Asn Leu Glu Ile His Asn Glu Arg
 500 505

<210> 173

<211> 505

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 173

Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala
 1 5 10 15
 Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30
 Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45
 Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu
 50 55 60
 Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly
 85 90 95
 Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys
 100 105 110
 Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125
 Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser
 130 135 140

Thr Gln His Leu Ser Pro Asp Asn Ile Phe Glu Thr Val Arg Lys Thr
 145 150 155 160
 Asn Asp Ser Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175
 His Gly Met Val Ala Phe Arg Asp Pro Phe Gly Ile Arg Pro Leu Val
 180 185 190
 Leu Gly Lys Arg Glu Ile Glu Gly Lys Thr Glu Tyr Met Phe Ala Ser
 195 200 205
 Glu Ser Val Ala Leu Asp Val Val Gly Phe Glu Phe Val Arg Asp Val
 210 215 220
 Leu Pro Gly Glu Ala Ile Tyr Val Thr Phe Asp Gly Gln Leu His Ser
 225 230 235 240
 Gln Ile Cys Ala Asp Asn Pro Lys Leu Asn Pro Cys Ile Phe Glu Tyr
 245 250 255
 Val Tyr Phe Ala Arg Pro Asp Ser Val Ile Asp Gly Val Ser Val Tyr
 260 265 270
 Ser Ala Arg Val His Met Gly Glu Leu Leu Gly Glu Lys Ile Lys Arg
 275 280 285
 Glu Trp Gly Arg Ile Ile Asp Asp Ile Asp Val Val Ile Pro Ile Pro
 290 295 300
 Glu Thr Ser Asn Asp Ile Ala Val Arg Ile Ala Asn Met Leu Tyr Lys
 305 310 315 320
 Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Ala Arg Thr Phe
 325 330 335
 Ile Met Pro Gly Gln Ala Gln Arg Lys Ser Ser Val Arg Arg Lys Leu
 340 345 350
 Asn Ala Ile Ala Ser Glu Phe Lys Gly Lys Ser Val Leu Val Asp
 355 360 365
 Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala
 370 375 380
 Arg Ala Ala Gly Ala Lys Arg Val Tyr Phe Ala Ser Ala Ala Pro Glu
 385 390 395 400
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu
 405 410 415
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly
 420 425 430
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile
 435 440 445
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr
 450 455 460
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile
 465 470 475 480

Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
 485 490 495

Thr Asn Leu Glu Ile His Asn Glu Arg
 500 505

<210> 174

<211> 386

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(384)

<220>

<223> yjgF

<400> 174

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 Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

gtg caa gca gtt gat tta ggc aat atg gtt tta act tct ggg caa att 96
 Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
 20 25 30

ccc gtg aat cct gaa acc ggc gaa atc ccg agt gat att gtg caa caa 144
 Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
 35 40 45

acc cgc caa tct ctg aac aac gtg aaa gcc att atc gaa caa gcc ggc 192
 Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
 50 55 60

tta acc gtt gcc gat att gta aag acc acc gta ttt gtc aaa gat ctt 240
 Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
 65 70 75 80

aac gac ttc gca aag gta aat gcg gaa tac caa gcc ttc ttc caa gaa 288
 Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
 85 90 95

aac gaa cac cct aat ttt ccg gct cgt tct tgc gta gaa gtg gct cgt 336
 Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
 100 105 110

tta cca aaa gat gtt ggc att gag atc gaa gcg att gca gta cgc cga 384
 Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
 115 120 125

ta 386

<210> 175

<211> 128

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 175

Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

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Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
      20                      25                      30
Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
      35                      40                      45
Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
      50                      55                      60
Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
      65                      70                      75                      80
Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
      85                      90                      95
Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
      100                     105                     110
Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
      115                     120                     125

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<210> 176

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223> Description of Artificial Sequence: PRIMER

<400> 176

atggcnggng cnaargarat

20

<210> 177

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223> Description of Artificial Sequence: PRIMER

<220>

<221> misc_feature

<222> 3

<223> n = A or T or G or C

<220>

<221> misc_feature

<222> 12

<223> n = A or T or G or C

<220>

<221> misc_feature

<222> 15

<223> n = A or T or G or C

<400> 177

gcngcyttca tngcnaccat

20

<210> 178

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
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<222> 3
<223> N = A or T or G or C

<400> 178
ggnTTYatYc ayaaaaayAT g 21

<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<400> 179
tcttTngtra tngtnacATc rtg 23

<210> 180
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 180
gcsggyaaac crcgTtgga ttgG 24

<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 181
crctgaarat rtctgaaagc accac 25

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<210> 182
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 9
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 18
<223> N = A or T or G or C

<400> 182
atgtgyggna tygtnggnat                                20

<210> 183
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 183
catatcaata ccatacacat t                                21

<210> 184
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<400> 184
ggnccntayg tncarg                                    16

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<210> 185
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 1
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 4
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 10
<223> N = A or T or G or C

<400> 185
ngcnacytcn acrca 15

<210> 186
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 186
gaagccgcc aacgctcttg gg 22

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 187
gttgcttctt ttgcttcac tgg 23

<210> 188
<211> 24
<212> DNA
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A61K 39/102, 35/74, C12N 15/31, 15/63, C07K 14/285,
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09/809,665 15 March 2001 (15.03.2001) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU,
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GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 02/01971

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N1/20 A61K39/102 A61K35/74 C12N15/31 C12N15/63
C07K14/285 C07K16/12 C12Q1/18 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, WPI Data, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL [Online] 10 February 2001 (2001-02-10) MAY B.J. ET AL.: "Pasteurella multocida PM70 section 152 of 204 of the complete genome" Database accession no. AE006064 XP002224305 nucleotides 3352-4146	1-41
X	& DATABASE EMBL [Online] Entry AE006064, 10 February 2001 (2001-02-10) MAY B.J. ET AL.: "Pasteurella multocida PM70 section 31 of 204 of the complete genome" the whole document	5-23,25, 28
A	& BARBARA J. MAY ET AL.: "Complete genomic sequence of Pasteurella multocida, Pm70" PROCEEDINGS OF THE NATIONAL ACADEMY OF -/--	1-41

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
 "E" earlier document but published on or after the international filing date
 "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
 "O" document referring to an oral disclosure, use, exhibition or other means
 "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
 "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
 "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
 "A" document member of the same patent family

Date of the actual completion of the international search

12 May 2003

Date of mailing of the international search report

16. 05. 2003

Name and mailing address of the ISA

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Authorized officer

Montero Lopez, B

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SCIENCES OF USA, vol. 98, no. 6, 13 March 2001 (2001-03-13), pages 3460-3465, XP002202785 WASHINGTON US page 3463, right-hand column, paragraph 2 -page 3464, left-hand column, paragraph 1 ---</p> <p>COONEY ET AL: "Three contiguous lipoprotein genes in Pasteurella haemolytica A1 which are homologous to a lipoprotein gene in Haemophilus influenza Type b" INFECTION AND IMMUNITY, AMERICAN SOCIETY OF MICROBIOLOGY, WASHINGTON, DC, US, vol. 61, no. 11, November 1993 (1993-11), pages 4682-4688, XP002148894 ISSN: 0019-9567 abstract page 4683, left-hand column, last paragraph -page 4685, left-hand column, paragraph 1; figures 3,4 page 4686, right-hand column, paragraph 2 ---</p>	5-23,25, 28
A	<p>TROY E. FULLER ET AL.: "Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis" MICROBIAL PATHOGENESIS, vol. 29, 2000, pages 25-38, XP002224304 the whole document -----</p>	1-41

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 02/01971**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-41 partially
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-41 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:1 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:1, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:2; antibody against it; use of the polypeptide of sequence SEQ ID NO:2 for identifying antibacterial agents.

2. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NO:3 and 4; 7 and 8; 9 and 10; 21 and 22; 25 and 26.

3. Claims: 1-4, 21-23, 27, 28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:27 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; nucleotide sequence comprising SEQ ID NO:27.

4. Claims: 1-41 partially

Idem as subject 1 for, respectively, sequences SEQ ID NOs:29 and 30; 39 and 40; 41 and 42; 51 and 52; 53 and 54; 55 and 56.

5. Claims: 1-28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:57 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:57.

6. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NOs:58 and 59; 60 and 61; 68 and 69; 72 and 73; 74 and 75; 76 and 77; 78 and 79; 80 and 81; 82 and 83; 84 and 85; 104 and 105; 108 and 109; 112 and 113; 116 and 117; 118 and 119; 120 and 121; 122 and 123; 124 and 125; 126 and 127; 128 and 129; 130 and 131

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

7. Claims: 5-26, 29-41 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in a gene of sequence SEQ ID NO:11; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:11, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:12; antibody against it; use of the polypeptide of sequence SEQ ID NO:12 for identifying antibacterial agents.

8. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:13 and 14; 15 and 16; 17 and 18; 19 and 20; 23 and 24; 31 and 32; 33 and 34; 35 and 36; 37 and 38; 70 and 71; 100 and 101; 102 and 103; 106 and 107; 110 and 111; 114 and 115; 132 and 133; 134 and 135; 136 and 137; 138 and 139; 140 and 141; 142 and 143; 144 and 145; 146 and 147; 148 and 149; 150 and 151; 152 and 153; 154 and 155; 156 and 157; 158 and 159; 160 and 161

9. Claims: 5-26 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in, respectively a gene of sequence SEQ ID NO:162 and 163; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:162 or 163.

10. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:164 and 165; 166 and 167; 168 and 169; 170 and 171; 172 and 173; 174 and 175

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A61K 39/102, 35/74, C12N 15/31, 15/63, C07K 14/285,
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(21) International Application Number: PCT/US02/01971

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09/809,665 15 March 2001 (15.03.2001) US(71) Applicant (for all designated States except US): PHAR-
MACIA & UPJOHN COMPANY [US/US]; 301 Henri-
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Battle Creek, MI 49014 (US). KENNEDY, Michael, J.
[US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).(74) Agent: WILLIAMS, Joseph, A., Jr.; Marshall, Gerstein
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Chicago, IL 60606 (US).(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,
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KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,
GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent
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- with amended claims

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For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

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AMENDED CLAIMS

[received by the International Bureau on 11 July 2003 (11.07.03)
original claims 1 to 41 have been amended by claims 1 to 29]

WHAT IS CLAIMED IS:

1. An attenuated *Mannheimia* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The *Mannheimia* bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The *Mannheimia* bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The *Mannheimia* bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. The *Mannheimia* bacteria of claim 1 wherein the *Mannheimia bacteria* is *Mannheimia haemolytica*.
6. The *Mannheimia* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Mannheimia* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
8. The *Mannheimia* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.
9. An immunogenic composition comprising the bacteria according to any one of claims 1 through 8.

10. A vaccine composition comprising the immunogenic composition according to claim 9 and a pharmaceutically acceptable carrier.

11. The vaccine composition according to claim 10 further comprising an
5 adjuvant.

12. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog
10 thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

13. A method for producing an attenuated *Mannheimia* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide
15 sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

14. A purified and isolated *Mannheimia* polynucleotide comprising a
20 nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOS: 166, 168, 170, 172 and 174.

15. A purified and isolated *Mannheimia* polynucleotide comprising a
nucleotide sequence as set forth in SEQ ID NO: 166.

25

16. A purified and isolated polynucleotide encoding a *Mannheimia* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 14;

b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a); and

c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

5

17. A purified and isolated *Mannheimia* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

10

18. The polynucleotide of claim 17 which is a DNA.

19. A vector comprising the DNA of claim 18.

20. The vector of claim 19 that is an expression vector, wherein the DNA
15 is operatively linked to an expression control DNA sequence.

21. A host cell stably transformed or transfected with the DNA of claim 18 in a manner allowing the expression of the encoded polypeptide in said host cell.

20

22. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 21 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

23. A purified polypeptide produced by the method of claim 22.

25

24. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

24. 25. An antibody that is specifically reactive with the polypeptide of claim 24.

26. The antibody of claim 25 that is a monoclonal antibody.

5

27. A method of using the monoclonal antibody of claim 26 for identifying a bacteria of claims 1 or 5, comprising the steps of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

10

28. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

15

29. A method of identifying an anti-bacterial agent comprising the steps of:

- 20 a) measuring expression or activity of a gene product as set out in any one of SEQ ID NOS: 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound;
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when
- 25 expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the absence of the test compound.